(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
17 April 2003 (17.04.2003)

PCT

(10) International Publication Number
WO 03/031464 A2

(51) International Patent Classification⁷: C07K

(21) International Application Number: PCT/US02/32263

(22) International Filing Date: 9 October 2002 (09.10.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/328,523	10 October 2001 (10.10.2001)	US
60/344,692	19 October 2001 (19.10.2001)	US
60/334,233	28 November 2001 (28.11.2001)	US
60/334,301	28 November 2001 (28.11.2001)	US
60/387,292	7 June 2002 (07.06.2002)	US
60/391,777	25 June 2002 (25.06.2002)	US
60/396,594	17 July 2002 (17.07.2002)	US
60/404,249	16 August 2002 (16.08.2002)	US
60/407,527	28 August 2002 (28.08.2002)	US

(71) Applicant *(for all designated States except US)*: **NEOSE TECHNOLOGIES, INC.** [US/US]; 102 Witmer Road, Horsham, PA 19044 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **DE FREES, Shawn** [US/US]; 126 Filly Drive, North Wales, PA 19454 (US). **ZOPF, David** [US/US]; 560 W. Beechtree Lane, Wayne, PA 19087 (US). **BAYER, Robert** [US/US]; 6105 Dirac Street, San Diego, CA 92122 (US). **BOWE, Caryn** [US/US]; 276 Cherry Lane, Doylestown, PA 18901 (US). **HAKES, David** [US/US]; 14 Fern Avenue, Willow Grove, PA 19090 (US). **CHEN, Xi** [CN/US]; 107 Whitney Place, Lansdale, PA 19446 (US).

(74) Agents: **DOYLE, Kathryn** et al.; Morgan, Lewis & Bockius, L.L.P., 1701 Market Street, Philadelphia, PA 19103 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT (utility model), AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ (utility model), CZ, DE, DK (utility model), DK, DM, DZ, EC, EE (utility model), EE, ES, FI (utility model), FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO utility model (GH), ARIPO patent (GH), ARIPO utility model (GM), ARIPO patent (GM), ARIPO utility model (KE), ARIPO patent (KE), ARIPO utility model (LS), ARIPO patent (LS), ARIPO utility model (MW), ARIPO patent (MW), ARIPO utility model (MZ), ARIPO patent (MZ), ARIPO utility model (SD), ARIPO patent (SD), ARIPO utility model (SL), ARIPO patent (SL), ARIPO utility model (SZ), ARIPO patent (SZ), ARIPO utility model (TZ), ARIPO patent (TZ), ARIPO utility model (UG), ARIPO patent (UG), ARIPO utility model (ZM), ARIPO patent (ZM), ARIPO utility model (ZW), ARIPO patent (ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 03/031464 A2

(54) Title: REMODELING AND GLYCOCONJUGATION OF PEPTIDES

(57) Abstract: The invention includes methods and compositions for remodeling a peptide molecule, including the addition or deletion of one or more glycosyl groups to a peptide, and/or the addition of a modifying group of peptide.

TITLE OF THE INVENTION

REMODELING AND GLYCOCONJUGATION OF PEPTIDES

BACKGROUND OF THE INVENTION

Most naturally occurring peptides contain carbohydrate moieties attached to the peptide via specific linkages to a select number of amino acids along the length of the primary peptide chain. Thus, many naturally occurring peptides are termed "glycopeptides." The variability of the glycosylation pattern on any given peptide has enormous implications for the function of that peptide. For example, the structure of the N-linked glycans on a peptide can impact various characteristics of the peptide, including the protease susceptibility, intracellular trafficking, secretion, tissue targeting, biological half-life and antigenicity of the peptide in a cell or organism. The alteration of one or more of these characteristics greatly affects the efficacy of a peptide in its natural setting, and also affects the efficacy of the peptide as a therapeutic agent in situations where the peptide has been generated for that purpose.

The carbohydrate structure attached to the peptide chain is known as a "glycan" molecule. The specific glycan structure present on a peptide affects the solubility and aggregation characteristics of the peptide, the folding of the primary peptide chain and therefore its functional or enzymatic activity, the resistance of the peptide to proteolytic attack and the control of proteolysis leading to the conversion of inactive forms of the peptide to active forms. Importantly, terminal sialic acid residues present on the glycan molecule affect the length of the half life of the peptide in the mammalian circulatory system. Peptides whose glycans do not contain terminal sialic acid residues are rapidly removed from the circulation by the liver, an event which negates any potential therapeutic benefit of the peptide.

The glycan structures found in naturally occurring glycopeptides are typically divided into two classes, N-linked and O-linked glycans.

Peptides expressed in eukaryotic cells are typically N-glycosylated on asparagine residues at sites in the peptide primary structure containing the sequence asparagine-X-

serine/threonine where X can be any amino acid except proline and aspartic acid. The carbohydrate portion of such peptides is known as an N-linked glycan. The early events of N-glycosylation occur in the endoplasmic reticulum (ER) and are identical in mammals, plants, insects and other higher eukaryotes. First, an oligosaccharide chain comprising fourteen sugar residues is constructed on a lipid carrier molecule. As the nascent peptide is translated and translocated into the ER, the entire oligosaccharide chain is transferred to the amide group of the asparagine residue in a reaction catalyzed by a membrane bound glycosyltransferase enzyme. The N-linked glycan is further processed both in the ER and in the Golgi apparatus. The further processing generally entails removal of some of the sugar residues and addition of other sugar residues in reactions catalyzed by glycosylases and glycosyltransferases specific for the sugar residues removed and added.

Typically, the final structures of the N-linked glycans are dependent upon the organism in which the peptide is produced. For example, in general, peptides produced in bacteria are completely unglycosylated. Peptides expressed in insect cells contain high mannose, paunci-mannose N-linked oligosaccharide chains, among others. Peptides produced in mammalian cell culture are usually glycosylated differently depending, e.g., upon the species and cell culture conditions. Even in the same species and under the same conditions, a certain amount of heterogeneity in the glycosyl chain is sometimes encountered. Further, peptides produced in plant cells comprise glycan structures that differ significantly from those produced in animal cells. The dilemma in the art of the production of recombinant peptides, particularly when the peptides are to be used as therapeutic agents, is to be able to generate peptides that are correctly glycosylated, i.e., to be able to generate a peptide having a glycan structure that resembles, or is identical to that present on the naturally occurring form of the peptide. Most peptides produced by recombinant means comprise glycan structures that are different from the naturally occurring glycans.

A variety of methods have been proposed in the art to customize the glycosylation pattern of a peptide including those described in WO 99/22764, WO 98/58964, WO 99/54342 and U.S. Patent No. 5,047,335, among others. Essentially, many of the enzymes required for the *in vitro* glycosylation of peptides have been cloned and sequenced. In some instances, these enzymes have been used *in vitro* to add specific sugars to an incomplete glycan molecule on a peptide. In other instances, cells have been genetically engineered to express a

combination of enzymes and desired peptides such that addition of a desired sugar moiety to an expressed peptide occurs within the cell.

Peptides may also be modified by addition of O-linked glycans, also called mucin-type glycans because of their prevalence on mucinous glycopeptide. Unlike N-glycans that are linked to asparagine residues and are formed by *en bloc* transfer of oligosaccharide from lipid-bound intermediates, O-glycans are linked primarily to serine and threonine residues and are formed by the stepwise addition of sugars from nucleotide sugars (Tanner *et al.*, *Biochim. Biophys. Acta.* **906**:81-91 (1987); and Hounsell *et al.*, *Glycoconj. J.* **13**:19-26 (1996)). Peptide function can be affected by the structure of the O-linked glycans present thereon. For example, the activity of P-selectin ligand is affected by the O-linked glycan structure present thereon. For a review of O-linked glycan structures, see Schachter and Brockhausen, The Biosynthesis of Branched O-Linked Glycans, 1989, Society for Experimental Biology, pp. 1-26 (Great Britain). Other glycosylation patterns are formed by linking glycosylphosphatidylinositol to the carboxyl-terminal carboxyl group of the protein (Takeda *et al.*, *Trends Biochem. Sci.* **20**:367-371 (1995); and Udenfriend *et al.*, *Ann. Rev. Biochem.* **64**:593-591 (1995).

Although various techniques currently exist to modify the N-linked glycans of peptides, there exists in the art the need for a generally applicable method of producing peptides having a desired, i.e., a customized glycosylation pattern. There is a particular need in the art for the customized *in vitro* glycosylation of peptides, where the resulting peptide can be produced at industrial scale. This and other needs are met by the present invention.

The administration of glycosylated and non-glycosylated peptides for engendering a particular physiological response is well known in the medicinal arts. Among the best known peptides utilized for this purpose is insulin, which is used to treat diabetes. Enzymes have also been used for their therapeutic benefits. A major factor, which has limited the use of therapeutic peptides is the immunogenic nature of most peptides. In a patient, an immunogenic response to an administered peptide can neutralize the peptide and/or lead to the development of an allergic response in the patient. Other deficiencies of therapeutic peptides include suboptimal potency and rapid clearance rates. The problems inherent in peptide therapeutics are recognized in the art, and various methods of eliminating the

problems have been investigated. To provide soluble peptide therapeutics, synthetic polymers have been attached to the peptide backbone.

Poly(ethylene glycol) ("PEG") is an exemplary polymer that has been conjugated to peptides. The use of PEG to derivatize peptide therapeutics has been demonstrated to reduce the immunogenicity of the peptides and prolong the clearance time from the circulation. For example, U.S. Pat. No. 4,179,337 (Davis *et al.*) concerns non-immunogenic peptides, such as enzymes and peptide hormones coupled to polyethylene glycol (PEG) or polypropylene glycol. Between 10 and 100 moles of polymer are used per mole peptide and at least 15% of the physiological activity is maintained.

WO 93/15189 (Veronese *et al.*) concerns a method to maintain the activity of polyethylene glycol-modified proteolytic enzymes by linking the proteolytic enzyme to a macromolecularized inhibitor. The conjugates are intended for medical applications.

The principal mode of attachment of PEG, and its derivatives, to peptides is a non-specific bonding through a peptide amino acid residue. For example, U.S. Patent No. 4,088,538 discloses an enzymatically active polymer-enzyme conjugate of an enzyme covalently bound to PEG. Similarly, U.S. Patent No. 4,496,689 discloses a covalently attached complex of α-1 protease inhibitor with a polymer such as PEG or methoxypoly(ethylene glycol) ("mPEG"). Abuchowski *et al.* (*J. Biol. Chem.* **252**: 3578 (1977) discloses the covalent attachment of mPEG to an amine group of bovine serum albumin. U.S. Patent No. 4,414,147 discloses a method of rendering interferon less hydrophobic by conjugating it to an anhydride of a dicarboxylic acid, such as poly(ethylene succinic anhydride). PCT WO 87/00056 discloses conjugation of PEG and poly(oxyethylated) polyols to such proteins as interferon-β, interleukin-2 and immunotoxins. EP 154,316 discloses and claims chemically modified lymphokines, such as IL-2 containing PEG bonded directly to at least one primary amino group of the lymphokine. U.S. Patent No. 4,055,635 discloses pharmaceutical compositions of a water-soluble complex of a proteolytic enzyme linked covalently to a polymeric substance such as a polysaccharide.

Another mode of attaching PEG to peptides is through the non-specific oxidation of glycosyl residues on a peptide. The oxidized sugar is utilized as a locus for attaching a PEG moiety to the peptide. For example M'Timkulu (WO 94/05332) discloses the use of a

hydrazine- or amino-PEG to add PEG to a glycoprotein. The glycosyl moieties are randomly oxidized to the corresponding aldehydes, which are subsequently coupled to the amino-PEG.

In each of the methods described above, poly(ethylene glycol) is added in a random, non-specific manner to reactive residues on a peptide backbone. For the production of therapeutic peptides, it is clearly desirable to utilize a derivatization strategy that results in the formation of a specifically labeled, readily characterizable, essentially homogeneous product.

Two principal classes of enzymes are used in the synthesis of carbohydrates, glycosyltransferases (*e.g.*, sialyltransferases, oligosaccharyltransferases, N-acetylglucosaminyltransferases), and glycosidases. The glycosidases are further classified as exoglycosidases (*e.g.*, β-mannosidase, β-glucosidase), and endoglycosidases (*e.g.*, Endo-A, Endo-M). Each of these classes of enzymes has been successfully used synthetically to prepare carbohydrates. For a general review, *see,* Crout *et al., Curr. Opin. Chem. Biol.* **2**: 98-111 (1998).

Glycosyltransferases modify the oligosaccharide structures on peptides. Glycosyltransferases are effective for producing specific products with good stereochemical and regiochemical control. Glycosyltransferases have been used to prepare oligosaccharides and to modify terminal N- and O-linked carbohydrate structures, particularly on peptides produced in mammalian cells. For example, the terminal oligosaccharides of glycopeptides have been completely sialylated and/or fucosylated to provide more consistent sugar structures, which improves glycopeptide pharmacodynamics and a variety of other biological properties. For example, β-1,4-galactosyltransferase is used to synthesize lactosamine, an illustration of the utility of glycosyltransferases in the synthesis of carbohydrates (*see, e.g.*, Wong *et al., J. Org. Chem.* **47**: 5416-5418 (1982)). Moreover, numerous synthetic procedures have made use of α-sialyltransferases to transfer sialic acid from cytidine-5'-monophospho-N-acetylneuraminic acid to the 3-OH or 6-OH of galactose (*see, e.g.*, Kevin *et al., Chem. Eur. J.* **2**: 1359-1362 (1996)). Fucosyltransferases are used in synthetic pathways to transfer a fucose unit from guanosine-5'-diphosphofucose to a specific hydroxyl of a saccharide acceptor. For example, Ichikawa prepared sialyl Lewis-X by a method that involves the fucosylation of sialylated lactosamine with a cloned fucosyltransferase (Ichikawa *et al., J. Am. Chem. Soc.* **114**: 9283-9298 (1992)). For a discussion of recent advances in glycoconjugate synthesis for therapeutic use *see,* Koeller *et al., Nature*

Biotechnology **18**: 835-841 (2000). *See* also, U.S. Patent No. 5,876,980; 6,030,815; 5,728,554; 5,922,577; and WO/9831826.

Glycosidases can also be used to prepare saccharides. Glycosidases normally catalyze the hydrolysis of a glycosidic bond. However, under appropriate conditions, they can be used to form this linkage. Most glycosidases used for carbohydrate synthesis are exoglycosidases; the glycosyl transfer occurs at the non-reducing terminus of the substrate. The glycosidase binds a glycosyl donor in a glycosyl-enzyme intermediate that is either intercepted by water to yield the hydrolysis product, or by an acceptor, to generate a new glycoside or oligosaccharide. An exemplary pathway using an exoglycosidase is the synthesis of the core trisaccharide of all N-linked glycopeptides, including the β-mannoside linkage, which is formed by the action of β-mannosidase (Singh *et al., Chem. Commun.* 993-994 (1996)).

In another exemplary application of the use of a glycosidase to form a glycosidic linkage, a mutant glycosidase has been prepared in which the normal nucleophilic amino acid within the active site is changed to a non-nucleophilic amino acid. The mutant enzyme does not hydrolyze glycosidic linkages, but can still form them. Such a mutant glycosidase is used to prepare oligosaccharides using an α-glycosyl fluoride donor and a glycoside acceptor molecule (Withers et al., U.S. Patent No. 5,716,812).

Although their use is less common than that of the exoglycosidases, endoglycosidases are also utilized to prepare carbohydrates. Methods based on the use of endoglycosidases have the advantage that an oligosaccharide, rather than a monosaccharide, is transferred. Oligosaccharide fragments have been added to substrates using *endo*-β-N-acetylglucosamines such as *endo*-F, *endo*-M (Wang *et al., Tetrahedron Lett.* **37**: 1975-1978); and Haneda *et al., Carbohydr. Res.* **292**: 61-70 (1996)).

In addition to their use in preparing carbohydrates, the enzymes discussed above are applied to the synthesis of glycopeptides as well. The synthesis of a homogenous glycoform of ribonuclease B has been published (Witte K. et al., J. Am. Chem. Soc. **119**: 2114-2118 (1997)). The high mannose core of ribonuclease B was cleaved by treating the glycopeptide with endoglycosidase H. The cleavage occurred specifically between the two core GlcNAc residues. The tetrasaccharide sialyl Lewis X was then enzymatically rebuilt on the remaining GlcNAc anchor site on the now homogenous protein by the sequential use of β-1,4-

galactosyltransferase, α-2,3-sialyltransferase and α-1,3-fucosyltransferase V. However, while each enzymatically catalyzed step proceeded in excellent yield, such procedures have not been adapted for the generation of glycopeptides on an industrial scale.

Methods combining both chemical and enzymatic synthetic elements are also known in the art. For example, Yamamoto and coworkers (*Carbohydr. Res.* **305**: 415-422 (1998)) reported the chemoenzymatic synthesis of the glycopeptide, glycosylated Peptide T, using an endoglycosidase. The N-acetylglucosaminyl peptide was synthesized by purely chemical means. The peptide was subsequently enzymatically elaborated with the oligosaccharide of human transferrin peptide. The saccharide portion was added to the peptide by treating it with an endo-β-N-acetylglucosaminidase. The resulting glycosylated peptide was highly stable and resistant to proteolysis when compared to the peptide T and N-acetylglucosaminyl peptide T.

The use of glycosyltransferases to modify peptide structure with reporter groups has been explored. For example, Brossmer *et al.* (U.S. Patent No. 5,405,753) discloses the formation of a fluorescent-labeled cytidine monophosphate ("CMP") derivative of sialic acid and the use of the fluorescent glycoside in an assay for sialyl transferase activity and for the fluorescent-labeling of cell surfaces, glycoproteins and peptides. Gross *et al.* (*Analyt. Biochem.* **186**: 127 (1990)) describe a similar assay. Bean *et al.* (U.S. Patent No. 5,432,059) discloses an assay for glycosylation deficiency disorders utilizing reglycosylation of a deficiently glycosylated protein. The deficient protein is reglycosylated with a fluorescent-labeled CMP glycoside. Each of the fluorescent sialic acid derivatives is substituted with the fluorescent moiety at either the 9-position or at the amine that is normally acetylated in sialic acid. The methods using the fluorescent sialic acid derivatives are assays for the presence of glycosyltransferases or for non-glycosylated or improperly glycosylated glycoproteins. The assays are conducted on small amounts of enzyme or glycoprotein in a sample of biological origin. The enzymatic derivatization of a glycosylated or non-glycosylated peptide on a preparative or industrial scale using a modified sialic acid has not been disclosed or suggested in the prior art.

Considerable effort has also been directed towards the modification of cell surfaces by altering glycosyl residues presented by those surfaces. For example, Fukuda and coworkers have developed a method for attaching glycosides of defined structure onto cell surfaces.

The method exploits the relaxed substrate specificity of a fucosyltransferase that can transfer fucose and fucose analogs bearing diverse glycosyl substrates (Tsuboi *et al., J. Biol. Chem.* **271**: 27213 (1996)).

Enzymatic methods have also been used to activate glycosyl residues on a glycopeptide towards subsequent chemical elaboration. The glycosyl residues are typically activated using galactose oxidase, which converts a terminal galactose residue to the corresponding aldehyde. The aldehyde is subsequently coupled to an amine-containing modifying group. For example, Casares *et al.* (*Nature Biotech.* **19**: 142 (2001)) have attached doxorubicin to the oxidized galactose residues of a recombinant MHCII-peptide chimera.

Glycosyl residues have also been modified to contain ketone groups. For example, Mahal and co-workers (*Science* **276**: 1125 (1997)) have prepared N-levulinoyl mannosamine ("ManLev"), which has a ketone functionality at the position normally occupied by the acetyl group in the natural substrate. Cells were treated with the ManLev, thereby incorporating a ketone group onto the cell surface. *See,* also Saxon *et al., Science* **287**: 2007 (2000); Hang *et al., J. Am. Chem. Soc.* **123**: 1242 (2001); Yarema *et al., J. Biol. Chem.* **273**: 31168 (1998); and Charter *et al., Glycobiology* **10**: 1049 (2000).

The methods of modifying cell surfaces have not been applied in the absence of a cell to modify a glycosylated or non-glycosylated peptide. Further, the methods of cell surface modification are not utilized for the enzymatic incorporation preformed modified glycosyl donor moiety into a peptide. Moreover, none of the cell surface modification methods are practical for producing glycosyl-modified peptides on an industrial scale.

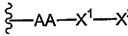
Despite the efforts directed toward the enzymatic elaboration of saccharide structures, there remains still a need for an industrially practical method for the modification of glycosylated and non-glycosylated peptides with modifying groups such as water-soluble polymers, therapeutic moieties, biomolecules and the like. Of particular interest are methods in which the modified peptide has improved properties, which enhance its use as a therapeutic or diagnostic agent. The present invention fulfills these and other needs.

SUMMARY OF THE INVENTION

The invention includes a multitude of methods of remodeling a peptide to have a specific glycan structure attached thereto. Although specific glycan structures are described herein, the invention should not be construed to be limited to any one particular structure. In addition, although specific peptides are described herein, the invention should not be limited by the nature of the peptide described, but rather should encompass any and all suitable peptides and variations thereof.

The description which follows discloses the preferred embodiments of the invention and provides a written description of the claims appended hereto. The invention encompasses any and all variations of these embodiments that are or become apparent following a reading of the present specification.

The invention includes a cell-free, in vitro method of remodeling a peptide having the formula:



wherein

AA is a terminal or internal amino acid residue of the peptide;

X^1-X^2 is a saccharide covalently linked to the AA, wherein

X^1 is a first glycosyl residue; and

X^2 is a second glycosyl residue covalently linked to X^1, wherein X^1 and X^2 are selected from monosaccharyl and oligosaccharyl residues. The method comprises:

(a) removing X^2 or a saccharyl subunit thereof from the peptide, thereby forming a truncated glycan; and

(b) contacting the truncated glycan with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer the at least one glycosyl donor to the truncated glycan, thereby remodeling the peptide.

In one aspect, the method further comprises

(c) removing X^1, thereby exposing the AA; and

(d) contacting the AA with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer the at least one glycosyl donor to the AA, thereby remodeling the peptide.

In another aspect, the method further comprises:

(e) prior to step (b), removing a group added to the saccharide during post-translational modification.

In one embodiment, the group is a member selected from phosphate, sulfate, carboxylate and esters thereof.

In another embodiment, the peptide has the formula:

wherein

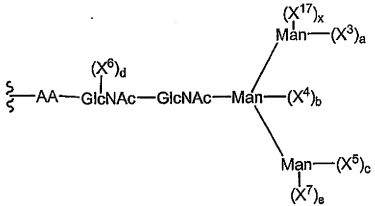
Z is a member selected from O, S, NH, and a crosslinker.

At least one of the glycosyl donors comprises a modifying group, and the modifying group may be a member selected from the group consisting of a water-soluble polymer, a therapeutic moiety, a detectable label, a reactive linker group, and a targeting moiety. Preferably, the modifying group is a water soluble polymer, and more preferably, the water soluble polymer comprises poly(ethylene glycol). Even more preferably, the poly(ethylene glycol) has a molecular weight distribution that is essentially homodisperse.

In this and several other embodiments, the peptide may be selected from the group consisting of granulocyte colony stimulating factor, interferon-alpha, interferon-beta, Factor VIIa, Factor IX, follicle stimulating hormone, erythropoietin, granulocyte macrophage colony stimulating factor, interferon-gamma, alpha-1-protease inhibitor, beta-glucosidase, tissue plasminogen activator protein, interleukin-2, Factor VIII, chimeric tumor necrosis

factor receptor, urokinase, chimeric anti-glycoproteinIIb/IIIa antibody, chimeric anti-HER2 antibody, chimeric anti-respiratory syncytial virus antibody, chimeric anti-CD20 antibody, DNase, chimeric anti-tumor necrosis factor antibody, human insulin, hepatitis B sAg, and human growth hormone.

Also included in the invention is a cell-free in vitro method of remodeling a peptide having the formula:



wherein

X^3, X^4, X^5, X^6, X^7 and X^{17} are independently selected monosaccharyl or oligosaccharyl residues; and

a, b, c, d, e, and x are independently selected from the integers 0, 1 and 2, with the proviso that at least one member selected from a, b, c, d, e, and x is 1 or 2. The method comprises:

(a) removing at least one of X^3, X^4, X^5, X^6, X^7 or X^{17}, or a saccharyl subunit thereof from the peptide, thereby forming a truncated glycan; and

(b) contacting the truncated glycan with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer the at least one glycosyl donor to the truncated glycan, thereby remodeling the peptide.

In one aspect, the removing of step (a) produces a truncated glycan in which a, b, c, e and x are each 0.

In another aspect, X^3, X^5 and X^7 are selected from the group consisting of $(mannose)_z$ and $(mannose)_z$-$(X^8)_y$

wherein

X^8 is a glycosyl moiety selected from mono- and oligo-saccharides;

y is an integer selected from 0 and 1; and

z is an integer between 1 and 20, wherein

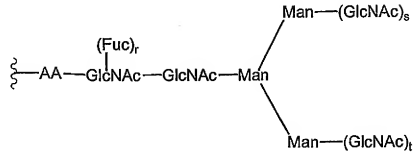
when z is 3 or greater, $(mannose)_z$ is selected from linear and branched structures.

In yet another aspect, X^4 is selected from the group consisting of GlcNAc and xylose. In a further aspect, wherein X^3, X^5 and X^7 are $(mannose)_u$, wherein u is selected from the integers between 1 and 20, and when u is 3 or greater, $(mannose)_n$ is selected from linear and branched structures.

At least one of the glycosyl donors comprises a modifying group, and the modifying group may be a member selected from the group consisting of a water-soluble polymer, a therapeutic moiety, a detectable label, a reactive linker group, and a targeting moiety. Preferably, the modifying group is a water soluble polymer, and more preferably, the water soluble polymer comprises poly(ethylene glycol). Even more preferably, the poly(ethylene glycol) has a molecular weight distribution that is essentially homodisperse.

In addition, the peptide may be selected from the group consisting of granulocyte colony stimulating factor, interferon-alpha, interferon-beta, Factor VIIa, Factor IX, follicle stimulating hormone, erythropoietin, granulocyte macrophage colony stimulating factor, interferon-gamma, alpha-1-protease inhibitor, beta-glucosidase, tissue plasminogen activator protein, interleukin-2, Factor VIII, chimeric tumor necrosis factor receptor, urokinase, chimeric anti-glycoproteinIIb/IIIa antibody, chimeric anti-HER2 antibody, chimeric anti-respiratory syncytial virus antibody, chimeric anti-CD20 antibody, DNase, chimeric anti-tumor necrosis factor antibody, human insulin, hepatitis B sAg, and human growth hormone.

Also included is a cell-free in vitro method of remodeling a peptide comprising a glycan having the formula:



wherein

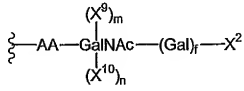
r, s, and t are integers independently selected from 0 and 1. The method comprises:

(a) contacting the peptide with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer the at least one glycosyl donor to the glycan, thereby remodeling the peptide.

In a preferred embodiment, at least one of the glycosyl donors comprises a modifying group, and the modifying group may be a member selected from the group consisting of a water-soluble polymer, a therapeutic moiety, a detectable label, a reactive linker group, and a targeting moiety. Preferably, the modifying group is a water soluble polymer, and more preferably, the water soluble polymer comprises poly(ethylene glycol). Even more preferably, the poly(ethylene glycol) has a molecular weight distribution that is essentially homodisperse.

Further, the peptide may be selected from the group consisting of granulocyte colony stimulating factor, interferon-alpha, interferon-beta, Factor VIIa, Factor IX, follicle stimulating hormone, erythropoietin, granulocyte macrophage colony stimulating factor, interferon-gamma, alpha-1-protease inhibitor, beta-glucosidase, tissue plasminogen activator protein, interleukin-2, Factor VIII, chimeric tumor necrosis factor receptor, urokinase, chimeric anti-glycoproteinIIb/IIIa antibody, chimeric anti-HER2 antibody, chimeric anti-respiratory syncytial virus antibody, chimeric anti-CD20 antibody, DNase, chimeric anti-tumor necrosis factor antibody, human insulin, hepatitis B sAg, and human growth hormone.

In yet another aspect, the peptide has the formula:

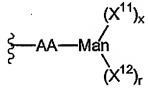


wherein

X^9 and X^{10} are independently selected monosaccharyl or oligosaccharyl residues; and

m, n and f are integers selected from 0 and 1.

In another aspect, the peptide has the formula:



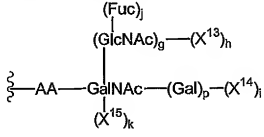
wherein

X^{11} and X^{12} are independently selected glycosyl moieties; and

r and x are integers independently selected from 0 and 1.

In a preferred embodiment, X^{11} and X^{12} are $(mannose)_q$, wherein q is selected from the integers between 1 and 20, and when q is three or greater, $(mannose)_q$ is selected from linear and branched structures.

In another aspect, the peptide has the formula:



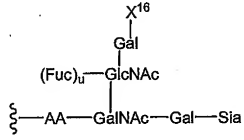
wherein

X^{13}, X^{14}, and X^{15} are independently selected glycosyl residues; and

g, h, i, j, k, and p are independently selected from the integers 0 and 1, with the proviso that at least one of g, h, i, j, k and p is 1.

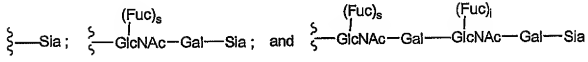
In one embodiment of this aspect of the invention, X^{14} and X^{15} are members independently selected from GlcNAc and Sia; and i and k are independently selected from the integers 0 and 1, with the proviso that at least one of i and k is 1, and if k is 1, g, h, and j are 0.

In another aspect of the invention, the peptide has the formula:



wherein

X^{16} is a member selected from:



wherein

s, u and i are independently selected from the integers 0 and 1.

On one embodiment of the invention the removing utilizes a glycosidase.

Also included in the invention is a cell-free, in vitro method of remodeling a peptide having the formula:

wherein

AA is a terminal or internal amino acid residue of the peptide;
X^1 is a glycosyl residue covalently linked to the AA, selected from monosaccharyl and oligosaccharyl residues; and
u is an integer selected from 0 and 1. The method comprises: contacting the peptide with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer the at least one glycosyl donor to the truncated glycan, wherein the glycosyl donor comprises a modifying group, thereby remodeling the peptide.

In a preferred embodiment, at least one of the glycosyl donors comprises a modifying group, and the modifying group may be a member selected from the group consisting of a water-soluble polymer, a therapeutic moiety, a detectable label, a reactive linker group, and a targeting moiety. Preferably, the modifying group is a water soluble polymer, and more preferably, the water soluble polymer comprises poly(ethylene glycol). Even more preferably, the poly(ethylene glycol) has a molecular weight distribution that is essentially homodisperse.

In addition, the peptide may be selected from the group consisting of granulocyte colony stimulating factor, interferon-alpha, interferon-beta, Factor VIIa, Factor IX, follicle stimulating hormone, erythropoietin, granulocyte macrophage colony stimulating factor, interferon-gamma, alpha-1-protease inhibitor, beta-glucosidase, tissue plasminogen activator protein, interleukin-2, Factor VIII, chimeric tumor necrosis factor receptor, urokinase, chimeric anti-glycoproteinIIb/IIIa antibody, chimeric anti-HER2 antibody, chimeric anti-respiratory syncytial virus antibody, chimeric anti-CD20 antibody, DNase, chimeric anti-tumor necrosis factor antibody, human insulin, hepatitis B sAg, and human growth hormone.

The invention additionally includes a covalent conjugate between a peptide and a modifying group that alters a property of the peptide, wherein the modifying group is covalently attached to the peptide at a preselected glycosyl or amino acid residue of the peptide via an intact glycosyl linking group.

In one aspect, the modifying group is a member selected from the group consisting of a water-soluble polymer, a therapeutic moiety, a detectable label, a reactive linker group, and a targeting moiety.

In another aspect, the modifying group and an intact glycosyl linking group precursor are bound as a covalently attached unit to the peptide via the action of an enzyme, the enzyme converting the precursor to the intact glycosyl linking group, thereby forming the conjugate.

The covalent conjugate of the invention comprises:

a first modifying group covalently bound to a first residue of the peptide via a first intact glycosyl linking group, and

a second glycosyl linking group bound to a second residue of the peptide via a second intact glycosyl linking group.

In one embodiment, the first residue and the second residue are structurally identical. In another embodiment, the first residue and the second residue have different structures. In an additional embodiment, the first residue and the second residue are glycosyl residues. In another embodiment, the first residue and the second residue are amino acid residues.

In yet another embodiment, the peptide is remodeled prior to forming the conjugate. Preferably, peptide is remodeled to introduce an acceptor moiety for the intact glycosyl linking group.

In another embodiment, the modifying group is a water-soluble polymer that may comprises poly(ethylene glycol), which, in another embodiment, may have a molecular weight distribution that is essentially homodisperse.

In yet a further embodiment, the peptide is selected from the group consisting of granulocyte colony stimulating factor, interferon-alpha, interferon-beta, Factor VIIa, Factor IX, follicle stimulating hormone, erythropoietin, granulocyte macrophage colony stimulating factor, interferon-gamma, alpha-1-protease inhibitor, beta-glucosidase, tissue

plasminogen activator protein, interleukin-2, Factor VIII, chimeric tumor necrosis factor receptor, urokinase, chimeric anti-glycoproteinIIb/IIIa antibody, chimeric anti-HER2 antibody, chimeric anti-respiratory syncytial virus antibody, chimeric anti-CD20 antibody, DNase, chimeric anti-tumor necrosis factor antibody, human insulin, hepatitis B sAg, and human growth hormone.

In another embodiment, the intact glycosyl linking unit is a member selected from the group consisting of a sialic acid residue, a Gal residue, a GlcNAc residue and a GalNAc residue.

There is also provided in the invention a method of forming a covalent conjugate between a polymer and a glycosylated or non-glycosylated peptide, wherein the polymer is conjugated to the peptide via an intact glycosyl linking group interposed between and covalently linked to both the peptide and the polymer. The method comprises contacting the peptide with a mixture comprising a nucleotide sugar covalently linked to the polymer and a glycosyltransferase for which the nucleotide sugar is a substrate under conditions sufficient to form the conjugate.

In a preferred embodiment, the polymer is a water-soluble polymer. In another preferred embodiment, the glycosyl linking group is covalently attached to a glycosyl residue covalently attached to the peptide, and in another embodiment, the glycosyl linking group is covalently attached to an amino acid residue of the peptide.

In yet a further embodiment, the polymer comprises a member selected from the group consisting of a polyalkylene oxide and a polypeptide. The polyalkylene oxide may be poly(ethylene glycol) in one embodiment of the invention. In another embodiment, the poly(ethylene glycol) has a degree of polymerization of from about 1 to about 20,000, preferably, from about 1 to about 5,000, or also preferably, the polyethylene glycol has a degree of polymerization of from about 1 to about 1,000.

In another embodiment, the glycosyltransferase is selected from the group consisting of sialyltransferase, galactosyltransferase, glucosyltransferase, GalNAc transferase, GlcNAc transferase, fucosyltransferase, and mannosyltransferase. In one

embodiment, the glycosyltransferase is recombinantly produced, and in another embodiment, the glycosyltransferase is a recombinant prokaryotic enzyme, or a recombinant eukaryotic enzyme.

In yet a further embodiment, the nucleotide sugar is selected from the group consisting of UDP-glycoside, CMP-glycoside, and GDP-glycoside and is preferably selected from the group consisting of UDP-galactose, UDP-galactosamine, UDP-glucose, UDP-glucosamine, UDP-N-acetylgalactosamine, UDP-N-acetylglucosamine, GDP-mannose, GDP-fucose, CMP-sialic acid, CMP-NeuAc.

In another embodiment, the peptide is a therapeutic agent.

In yet another embodiment, the glycosylated peptide is partially deglycosylated prior to the contacting.

In a further embodiment, the intact glycosyl linking group is a sialic acid residue.

Further, the method may be performed in a cell-free environment.

And, in another embodiment, the covalent conjugate may be isolated, and preferably, the covalent conjugate is isolated by membrane filtration.

There is also provided a method of forming a covalent conjugate between a first glycosylated or non-glycosylated peptide, and a second glycosylated or non-glycosylated peptide cojoined by a linker moiety, wherein

the linker moiety is conjugated to the first peptide via a first intact glycosyl linking group interposed between and covalently linked to both the first peptide and the linker moiety, and

the linker moiety is conjugated to the second peptide via a second intact glycosyl linking group interposed between and covalently linked to both the second peptide and the linker moiety. The method comprises:

(a) contacting the first peptide with a derivative of the linker moiety precursor comprising a precursor of the first intact glycosyl linking group and a precursor of the second intact glycosyl linking group;

(b) contacting the mixture from (a) with a glycosyl transferase for which the precursor of the first glycosyl linking group is a substrate, under conditions sufficient to convert the precursor of the first intact glycosyl linking group into the first intact glycosyl linking group, thereby forming a first conjugate between the linker moiety precursor and the first peptide;

(c) contacting the first conjugate with the second peptide and a glycosyltransferase for which the precursor of the second intact glycosyl group is a substrate under conditions sufficient to convert the precursor of the second intact glycosyl linking group into the second glycosyl linking group, thereby forming the conjugate between the linker moiety and the first glycosylated or non-glycosylated peptide, and the second glycosylated or non-glycosylated peptide.

In one aspect, the linker moiety comprises a water-soluble polymer, and in one embodiment, the water-soluble polymer comprises poly(ethylene glycol).

There is also provided a method of forming a covalent conjugate between a first glycosylated or non-glycosylated peptide, and a second glycosylated or non-glycosylated peptide cojoined by a linker moiety, wherein

the linker moiety is covalently conjugated to the first peptide, and

the linker moiety is conjugated to the second peptide via an intact glycosyl linking group interposed between and covalently linked to both the second peptide and the linker moiety. The method comprises:

(a) contacting the first peptide with an activated derivative of the linker moiety comprising;

a reactive functional group of reactivity complementary to a residue on the first peptide, and a precursor of the intact glycosyl linking group,

under conditions sufficient to form a covalent bond between the reactive functional group and the residue, thereby forming a first conjugate; and

(b) contacting the first conjugate with the second peptide and a glycosyltransferase for which the precursor of the intact glycosyl linking group is a substrate, under conditions sufficient to convert the precursor of the intact glycosyl linking group into the intact glycosyl linking group, thereby forming the conjugate between the first glycosylated or non-glycosylated peptide, and the second glycosylated or non-glycosylated peptide cojoined by the linker moiety.

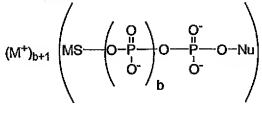
In one embodiment the linker moiety comprises a water-soluble polymer, which may be poly(ethylene glycol).

Also provided is a pharmaceutical composition comprising a pharmaceutically acceptable diluent and a covalent conjugate between a polymer and a glycosylated or non-glycosylated peptide, wherein the polymer is conjugated to the peptide via an intact glycosyl linking group interposed between and covalently linked to both the peptide and the polymer.

The invention further includes a composition for forming a conjugate between a peptide and a modified sugar, the composition comprising: an admixture of a modified sugar, a glycosyltransferase, and a peptide acceptor substrate, wherein the modified sugar has covalently attached thereto a member selected from a polymer, a therapeutic moiety and a biomolecule.

The invention also includes peptides remodeled using the methods of the invention and pharmaceutical compositions comprising the remodeled peptides.

Also provided in the invention is a compound having the formula:



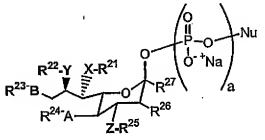
wherein

MS is a modified sugar comprising a sugar covalently bonded to a modifying group;

Nu is a nucleoside; and

b is an integer from 0 to 2.

In one aspect, there is included a compound having the formula:



wherein

X, Y, Z, A and B are members independently selected from S, O and NH;

R^{21}, R^{22}, R^{23}, R^{24}, and R^{25} members independently selected from H and a polymer;

R^{26} is a member selected from H, OH, and a polymer;

R^{27} is a member selected from COO^- and Na^+;

Nu is a nucleoside; and

a is an integer from 1 to 3.

The invention further provides a cell-free, in vitro method of remodeling a peptide having the formula:

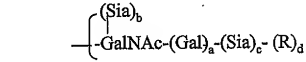
wherein

AA is a terminal or internal amino acid residue of the peptide. The method comprises:

contacting the peptide with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer the at least one glycosyl donor to the amino acid residue, wherein the glycosyl donor comprises a modifying group, thereby remodeling the peptide.

In each of the embodiments that are discussed below, specific remodeling schemes and peptides are identified solely to emphasize preferred embodiments of the invention.

The invention therefore includes a method of forming a conjugate between a granulocyte colony stimulating factor (G-CSF) peptide and a modifying group, wherein the modifying group is covalently attached to the G-CSF peptide through an intact glycosyl linking group, the G-CSF peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, and e are members independently selected from 0 and 1;

d is 0; and

R is a modifying group, a mannose or an oligomannose. The method comprises:

(a) contacting the G-CSF peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method further comprises:

(b) prior to step (a), contacting the G-CSF peptide with a sialidase under conditions appropriate to remove sialic acid from the G-CSF peptide.

In another embodiment, the method further comprises:

(c) prior to step (a), contacting the G-CSF peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the G-CSF peptide.

In yet another embodiment, the method further comprises:

(d) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In another embodiment, the method further comprises:

(e) prior to step (a), contacting the G-CSF peptide with N-acetylgalactosamine transferase and a GalNAc donor under conditions appropriate to transfer GalNAc to the G-CSF peptide.

In a further embodiment, the method further comprises:

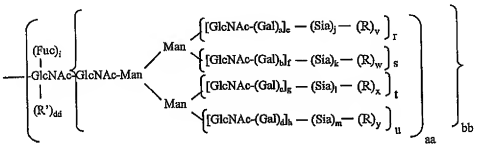
(f) prior to step (a), contacting the G-CSF peptide with endo-N-acetylgalactosaminidase operating synthetically and a GalNAc donor under conditions appropriate to transfer GalNAc to the G-CSF peptide.

In yet a further embodiment, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

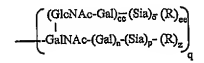
In specific embodiments, referring to the G-CSF peptide formula presented above, a, b, c, and e are 0. Alternatively, a and e are members independently selected from 0 and 1; and b, c, and d are 0. Alternatively, a, b, c, d, and e are members independently selected from 0 and 1.

The invention further includes a G-CSF peptide conjugate formed by the above-described methods.

There is also included a method of forming a conjugate between an interferon alpha peptide and a modifying group, wherein the modifying group is covalently attached to the glycopeptide through an intact glycosyl linking group, the glycopeptide comprising a glycosyl residue having a formula selected from:



; and



wherein

a, b, c, d, i, n, o, p, q, r, s, t, u, aa, bb, cc, dd, and ee are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers from 0 to 6;

j, k, l, and m are members independently selected from the integers from 0 to 20;

v, w, x, y, and z are 0; and

R is a modifying group, a mannose or an oligomannose

R' is H, a glycosyl residue, a modifying group, or a glycoconjugate.

The method comprises:

(a) contacting the glycopeptide with a member selected from a glycosyltransferase, an endo-acetylgalactosaminidase operating synthetically and a trans-sialidase, and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under

conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method further comprises:

(b) prior to step (a), contacting the glycopeptide with a sialidase under conditions appropriate to remove sialic acid from the glycopeptide.

In another embodiment, the method further comprises:

(c) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In yet an additional embodiment, the method further comprises:

(d) prior to step (a) contacting the glycopeptide with a combination of a glycosidase and a sialidase.

In an additional embodiment, the method further comprises:

(e) prior to step (a), contacting the glycopeptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

In yet another embodiment, the method also comprises:

(f) prior to step (a), contacting the glycopeptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the glycopeptide.

In addition, the method also comprises:

(g) prior to step (a), contacting the glycopeptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer galactose to the product.

Also, the method further comprises:

(h) prior to step (b), contacting the glycopeptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

The invention also further comprises:

(i) prior to step (a), contacting the glycopeptide with a mannosidase under conditions appropriate to remove mannose from the glycopeptide.

In addition, the method further comprises:

(j) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

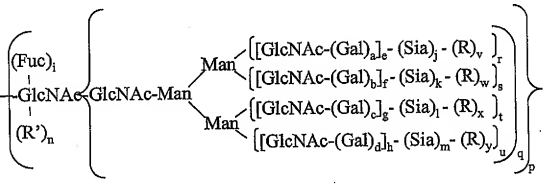
In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

According to the invention and with respect to the interferon alpha peptide formula disclosed above, a, b, c, d, aa, and bb are 1; e, f, g, and h are members independently selected from the integers from 1 to 4; i, j, k, l, m, r, s, t, u, and cc are members independently selected from 0 and 1; and n, o, p, q, v, w, x, y, z, dd, and ee are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, n, o, p, q, s, u, v, w, x, y, z, cc, dd, and ee are 0; e, g, i, r, and t are members independently selected from 0 and 1; and aa and bb are 1. Alternatively, a, b, c, d, e, f, g, i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; h is a member independently selected from the integers from 1 to 3; dd, v, w, x, and y are 0; and aa and bb are 1. Alternatively, a, b, c, d, f, h, j, k, l, m, s, u, v, w, x, y, and dd are 0; e, g, i, r, and t are members independently selected from 0 and 1; and aa and bb are 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, and dd are 0; r, s, t, u, v, w, x, and y are members independently selected from 0 and 1; and aa and bb are 1. Alternatively, a, b, c, d, e, f, g, h, i, r, s, t, and u are members independently selected from 0 and 1; j, k, l, m, v, w, x, y, and dd are 0; and aa and bb are 1. Alternatively, a, b, c, d, e, f, g, i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; h is a member independently selected from the integers from 1 to 3; v, w, x, y, and dd are 0; and aa and bb are 1. Alternatively, a, b, c, d, f, h, j, k, l, m, s, u, v, w, x, y, and dd are 0; e, g, i, r, and t are members independently selected from 0 and 1; and aa and bb are 1. Alternatively, n, o, and p are members independently selected from 0 and 1; q is 1; and z, cc, and ee are 0. Alternatively, n and q are members independently selected from 0 and 1; and o, p, z, cc, and ee are 0. Alternatively, n is 0 or 1; q is 1; and o, p, z, cc, and ee are 0. Alternatively, n, o, p, and f are members independently selected from 0 and 1; q is 1; and z

and ee are 0. Alternatively, n, o, p, and q are members independently selected from 0 and 1; and z, cc, and ee are 0. Alternatively, n and q are members independently selected from 0 and 1; and o, p, z, cc, and ee are 0. Alternatively, n, o, p, q, z, cc, and ee are 0.

There is also provided an interferon alpha peptide conjugate formed by the disclosed method.

The invention also includes a method of forming a conjugate between an interferon beta peptide and a modifying group, wherein the modifying group is covalently attached to the interferon beta peptide through an intact glycosyl linking group, the interferon beta peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, p, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0;

R is a modifying group, mannose or oligomannose; and

R' is H or a glycosyl, modifying group or glycoconjugate group. the method comprises:

(a) contacting the interferon beta peptide with a member selected from a glycosyltransferase and a trans-sialidase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method further comprises:

(b) prior to step (a), contacting the interferon beta peptide with a sialidase under conditions appropriate to remove sialic acid from the interferon beta peptide.

In another embodiment, the method further comprises:

(c) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In yet another embodiment, the method also further comprises:

(d) prior to step (a) contacting the interferon beta peptide with a combination of a glycosidase and a sialidase.

In an additional embodiment, the method further comprises:

(e) prior to step (a), contacting the interferon beta peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the interferon beta peptide.

Also, the method further comprises:

(f) prior to step (a), contacting the interferon beta peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the interferon beta peptide.

Additionally, the method also further comprises:

(g) prior to step (a), contacting the interferon beta peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer galactose to the product.

In yet another embodiment, the method further comprises:

(h) prior to step (b), contacting the interferon beta peptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the interferon beta peptide.

In yet a further embodiment, the method further comprises:

(i) prior to step (a), contacting the interferon beta peptide with a mannosidase under conditions appropriate to remove mannose from the interferon beta peptide.

In addition, the method further comprises:

(j) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

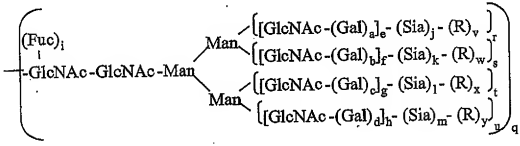
In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the beta interferon peptide formula disclosed above, h is a member independently selected from the integers between 1 and 3; a, b, c, d, e, f, g, i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; n, v, w, x, and y are 0; and q, p are 1. Alternatively, a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; e, g, i, r, and t are members independently selected from 0 and 1; and q, p are 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, r, s, t, u, v, w, x, and y are 0; q, p are 1; and i is independently selected from 0 and 1. Alternatively, a, b, c, d, e, f, g, h, I, j, k, l, m, r, s, t, u, v, w, x, and y are 0; and p, q are 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, and n are 0; q, p are 1; and r, s, t, u, v, w, x, and y are members independently selected from 0 and 1. Alternatively, a, b, c, d, e, f, g, h, i, r, s, t, and u are members independently selected from 0 and 1; j, k, l, m, n, v, w, x, and y are 0; and q, p are 1. Alternatively, wherein a, b, c, d, h, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; e, f, g, are members selected from the integers between 0 and 3; n, v, w, x, and y are 0; and q, p are 1.

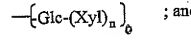
Alternatively, a, b, c, d, i, j, k, l, m, r, s, t, u, p and q are members independently selected from 0 and 1; e, f, g, and h are 1; and n, v, w, x, and y are 0.

Further included is an interferon beta peptide conjugate formed by the above-described method.

The invention also provides a method of forming a conjugate between a Factor VIIa peptide and a modifying group, wherein the modifying group is covalently attached to the Factor VIIa peptide through an intact glycosyl linking group, the Factor VIIa peptide comprising a glycosyl residue having a formula which is a member selected from:



; and



wherein

a, b, c, d, i, o, p, q, r, s, t, and u, are members independently selected from 0 and 1;

e, f, g, h and n are members independently selected from the integers from 0 to 6;

j, k, l and m are members independently selected from the integers from 0 to 20;

v, w, x and y are 0; and

R is a modifying group, a mannose, an oligomannose, SialylLewis^x or SialylLewis^a.

The method comprises:

(a) contacting the Factor VIIa peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying

group, under conditions appropriate for the formation of the intact glycosyl linking group.

In a preferred embodiment, the method further comprises:

(b) prior to step (a), contacting the Factor VIIa peptide with a sialidase under conditions appropriate to remove sialic acid from the Factor VIIa peptide.

In yet another preferred embodiment, the method comprises:

(c) prior to step (a), contacting the Factor VIIa peptide with a galactosidase under conditions appropriate to remove galactose from the Factor VIIa peptide.

In another embodiment, the method comprises:

(d) prior to step (a), contacting the Factor VIIa peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the Factor VIIa peptide.

In an additional embodiment, the method comprises:

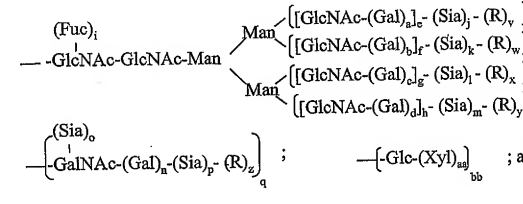
(e) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments, and referring to the Factor VIIa peptide formula disclosed above, a, b, c, d, e, g, i, j, l, o, p and q members independently selected from 0 and 1; r and t are 1; f, h, k, m, s, u, v, w, x and y are 0; and n is selected from the integers from 0 to 4. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, n, ,o, p, q, r, s, t and u are members independently selected from 0 and 1; v, w, x and y are 0; and n is a member selected from the integers from 0 to 4.

In addition, there is included a Factor VIIa peptide conjugate formed by the method disclosed herein.

The invention additionally provides a method of forming a conjugate between a Factor IX peptide and a modifying group, wherein the modifying group is covalently attached to the Factor IX peptide through an intact glycosyl linking group, the Factor IX peptide comprising a glycosyl residue having a formula which is a member selected from:



wherein

a, b, c, d, i, n, o, p, q, r, s, t, u, bb, cc, dd, ee, ff and gg are members independently selected from 0 and 1;

e, f, g, h and aa are members independently selected from the integers from 0 to 6;

j, k, l and m are members independently selected from the integers from 0 to 20;

v, w, x, y and z are 0;

R is a modifying group, a mannose or an oligomannose. The method comprises

(a) contacting the Factor IX peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group,

under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method further comprises:

(b) prior to step (a), contacting the Factor IX peptide with a sialidase under conditions appropriate to remove sialic acid from the Factor IX peptide.

In another embodiment, the method further comprises: (c) contacting the product formed in step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

Additionally, the method comprises:

(d) contacting the product from step (b) with a galactosyltransferase and a galactose donor under conditions appropriate to transfer the galactose to the product.

Moreover, the method comprises:

(e) contacting the product from step (d) with ST3Gal3 and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method further comprises:

(d) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

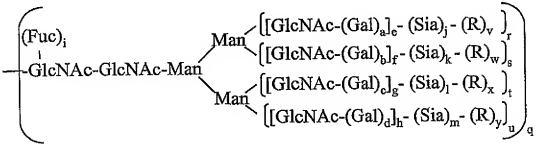
Also included is the fact that the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In additional embodiments and referring to the Factor IX peptide formula disclosed above, a, b, c, and d are 1; e, f, g and h are members independently selected from the integers from 1 to 4; aa, bb, cc, dd, ee, ff, j, k, l, m, i, n, o, p, q, r, s, t and u are members independently selected from 0 and 1; and v, w, x, y, z and gg are 0. Alternatively, a, b, c, d,

n, q are independently selected from 0 and 1; aa, e, f, g and h are members independently selected from the integers from 1 to 4; bb, cc, dd, ee, ff, j, k, l, m, i, o, p, r, s, t and u are members independently selected from 0 and 1; and v, w, x, y, z and gg are 0. Alternatively, a, b, c, d, n, bb, cc, dd and ff are 1; e, f, g, h and aa are members independently selected from the integers from 1 to 4; q, ee, i, j, k, l, m, o, p, r, s, t and u are members independently selected from 0 and 1; and v, w, x, y, z and gg are 0. Alternatively, a, b, c, d and q are 1; e, f, g and h are members independently selected from the integers from 1 to 4; aa, bb, cc, dd, ee, ff, j, k, l, m, i, n, o, p, r, s, t and u are members independently selected from 0 and 1; and v, w, x, y, z and gg are 0. Alternatively, a, b, c, d, q, bb, cc, dd and ff are 1; aa, e, f, g and h are members independently selected from the integers from 1 to 4; ee, i, j, k, l, m, o, p, r, s, t and u are members independently selected from 0 and 1; and v, w, x, y, z and gg are 0.

Also included is a Factor IX peptide conjugate formed by the above disclosed method.

The invention also provides a method of forming a conjugate between a follicle stimulating hormone (FSH) peptide and a modifying group, wherein the modifying group is covalently attached to the FSH peptide through an intact glycosyl linking group, the FSH peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0; and

R is a modifying group, a mannose or an oligomannose. The method comprises:

(a) contacting the FSH peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the FSH peptide with a sialidase under conditions appropriate to remove sialic acid from the FSH peptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the FSH peptide with a galactosidase under conditions appropriate to remove galactose from the FSH peptide.

In an additional embodiment, the method comprises:

(e) prior to step (a) contacting the FSH peptide with a combination of a glycosidase and a sialidase.

In yet a further embodiment, the method comprises:

(f) prior to step (a), contacting the FSH peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the FSH peptide.

In another embodiment, the method comprises:

(d) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In a further embodiment, the method comprises:

(e) prior to step (b), contacting the FSH peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the FSH peptide.

In another embodiment, the method comprises:

(f) prior to step (a), contacting the FSH peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the FSH peptide.

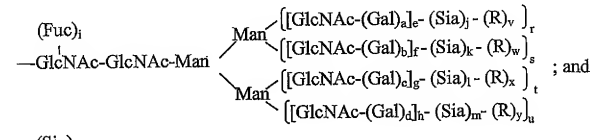
In yet another embodiment, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In additional preferred embodiments and referring to the FSH peptide formula described above, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; e, f, g, and h are 1; and v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m , s, u, v, w, x, and y are 0; and e, g, i, q, r, and t are members independently selected from 0 and 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, and m are 0; i, q, r, s, t, u, v, w, x, and y are independently selected from 0 and 1; p is 1; R (branched or linear) is a member selected from mannose and oligomannose. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, r, s, t, u, v, w, and y are 0; i is 0 or 1; and q is 1.

Also included is a FSH peptide conjugate formed by the above-described method.

The invention further provides a method of forming a conjugate between an erythropoietin (EPO) peptide and a modifying group, wherein the modifying group is covalently attached to the EPO peptide through an intact glycosyl linking group, the

EPO peptide comprising a glycosyl residue having a formula which is a member selected from:



; and

wherein

a, b, c, d, i, n, o, p, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 4;

j, k, l, and m are members independently selected from the integers between 0 and 20;

v, w, x, y, and z are 0; and

R is a modifying group, a mannose or an oligomannose. The method comprises:

(a) contacting the EPO peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the EPO peptide with a sialidase under conditions appropriate to remove sialic acid from the EPO peptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the EPO peptide with a galactosidase operating synthetically under conditions appropriate to add a galactose to the EPO peptide.

In an additional embodiment, the method comprises:

(e) prior to step (a), contacting the EPO peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the EPO peptide.

In a further embodiment, the method comprises:

(f) contacting the product from step (e) with ST3Gal3 and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

Additionally, the method comprises:

(g) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

Also, the method comprises:

(h) prior to step (a), contacting the EPO peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the EPO peptide.

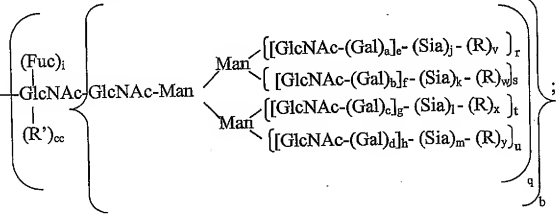
In another aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiment, and referring to the EPO peptide formula above, a, b, c, d, e, f, g, n, and q are 1; h is a member selected from the integers between 1 and 3; i, j, k,

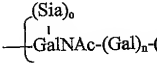
l, m, o, p, r, s, t, and u are members independently selected from 0 and 1; and, v, w, x, y and z are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, q, s, u, v, w, x, y, and z are 0; and e, g, i, r, and t are members independently selected from 0 and 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, n, o, p, q, r, s, t, and u are members independently selected from 0 and 1; and v, w, x, y, and z are 0. Alternatively, a, b, c, d, e, f, g, n, and q are 1; h is a member selected from the integers between 1 and 3; i, j, k, l, m, o, p, r, s, t, and u are members independently selected from 0 and 1; and v, w, x, y and z are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, o, p, s, u, v, w, x, y, and z are 0; and e, g, i, n, q, r, and t are independently selected from 0 and 1. Alternatively, a, b, c, d, f, h, j, k, l, m, n, o, p, s, u, v, w, x, y, and z are 0; and e, g, i, q, r, and t are members independently selected from 0 and 1. Alternatively, q is 1; a, b, c, d, e, f, g, h, i, n, r, s, t, and u are members independently selected from 0 and 1; and j, k, l, m, o, p, v, w, x, y, and z are 0.

Also included is an EPO peptide conjugate formed by the above-described method.

The invention further provides a method of forming a conjugate between a granulocyte macrophage colony stimulating factor (GM-CSF) peptide and a modifying group, wherein the modifying group is covalently attached to the GM-CSF peptide through an intact glycosyl linking group, the GM-CSF peptide comprising a glycosyl residue having a formula selected from:



; and



wherein

a, b, c, d, i, n, o, p, q, r, s, t, u, aa, bb, and cc are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0;

R is a modifying group, mannose or oligomannose; and

R' is H or a glycosyl residue, or a modifying group or a glycoconjugate. The method comprises:

(a) contacting the GM-CSF peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the GM-CSF peptide with a sialidase under conditions appropriate to remove sialic acid from the GM-CSF peptide.

In another embodiment, the method comprises:

(c) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In yet another embodiment, the method comprises:

(d) prior to step (a) contacting the GM-CSF peptide with a combination of a glycosidase and a sialidase.

In an additional embodiment, the method comprises:

(e) prior to step (a), contacting the GM-CSF peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the GM-CSF peptide.

Also, the method comprises:

(f) prior to step (a), contacting the GM-CSF peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the GM-CSF peptide.

Additionally, the method comprises:

(g) prior to step (a) contacting the GM-CSF peptide with a mannosidase under conditions appropriate to cleave a mannose residue from the GM-CSF peptide.

Further, the method comprises:

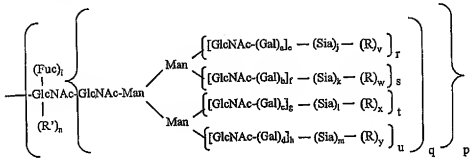
(h) prior to step (a), contacting the GM-CSF peptide with ST3Gal3 and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In additional preferred embodiments and referring to the GM-CSF peptide formula described above, a, b, c, d, i, j, k, l, m, o, p, q, r, s, t, u, and aa are members independently selected from 0 and 1; bb, e, f, g, h, and n are 1; and cc, v, w, x, y, and z are 0. Alternatively, a, b, c, d, i, j, k, l, m, o, p, q, r, s, t, u, and aa are members independently selected from 0 and 1; bb, e, f, g, h, and n are members independently selected from 0 and 1; and cc, v, w, x, y, and z are 0. Alternatively, cc, a, b, c, d, f, h, j, k, l, m, o, p, s, u, v, w, x, y, and z are 0; and e, g, i, n, q, r, t, and aa are members independently selected from 0 and 1; and bb is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, n, o, p, z and cc are 0; q, r, s, t, u, v, w, x, y, and aa are members independently selected from 0 and 1; bb is 1; and R is mannose or oligomannose. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, o, q, r, s, t, u, aa, and bb are members independently selected from 0 and 1; and n, p, v, w, x, y, z, and cc are 0.

Further included is a GM-CSF peptide conjugate formed by the above-described method.

The invention also includes a method of forming a conjugate between an interferon gamma peptide and a modifying group, wherein the modifying group is covalently attached to the interferon gamma peptide through an intact glycosyl linking group, the interferon gamma peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, n, p, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0;

R is a modifying group, mannose or oligomannose; and

R' is H or a glycosyl residue, a glycoconjugate, or a modifying group.

The method comprises:

(a) contacting the interferon gamma peptide with a member selected from a glycosyltransferase and a galactosidase operating synthetically and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying

group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the interferon gamma peptide with a sialidase under conditions appropriate to remove sialic acid from the interferon gamma peptide.

In another embodiment, the method comprises:

(c) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In an additional embodiment, the method comprises:

(d) prior to step (a) contacting the interferon gamma peptide with a combination of a glycosidase and a sialidase.

The method also comprises:

(e) prior to step (a), contacting the interferon gamma peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the interferon gamma peptide.

Additionally, the method comprises:

(f) prior to step (a), contacting the interferon gamma peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the interferon gamma peptide.

Also, the method comprises:

(g) prior to step (a), contacting the interferon gamma peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer galactose to the product.

In a further embodiment, the method comprises:

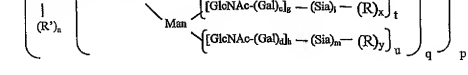
(h) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In another aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

Additional preferred embodiments include, referring to the interferon gamma interferon peptide formula above, where a, b, c, d, i, j, k, l, m, q, p, r, s, t, and u are members independently selected from 0 and 1; e, f, g, and h are 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; p, q, e, f, g, and h are 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and e, g, i, q, r, and t are members independently selected from 0 and 1; and p is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, and n are 0; q, r, s, t, u, v, w, x, and y are members independently selected from 0 and 1; and p is 1; and R is mannose or oligomannose. Alternatively, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; e, f, g, h, and p are 1; and n, v, w, x, and y are 0.

Further included is an interferon gamma peptide conjugate formed by the above-described method.

The invention further includes a method of forming a conjugate between an alpha 1 protease inhibitor (A-1-PI) peptide and a modifying group, wherein the modifying group is covalently attached to the A-1-PI peptide through an intact glycosyl linking group, the A-1-PI peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, n, p, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0;

R is a modifying group, mannose and oligomannose; and

R' is H or a glycosyl residue, a glycoconjugate, or a modifying group.

The method comprises:

(a) contacting the A-1-PI peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the A-1-PI peptide with a sialidase under conditions appropriate to remove sialic acid from the A-1-PI peptide.

In another embodiment, the method comprises:

(c) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

The method also comprises:

(d) prior to step (a) contacting the A-1-PI peptide with a combination of a glycosidase and a sialidase.

In addition, the method comprises:

(e) prior to step (a), contacting the A-1-PI peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the A-1-PI peptide.

In yet another embodiment, the method comprises:

(f) prior to step (a), contacting the A-1-PI peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the A-1-PI peptide.

Additionally, the method comprises:

(g) prior to step (a), contacting the A-1-PI peptide with a mannosidase under conditions appropriate to remove mannose from the A-1-PI peptide.

Further, the method comprises:

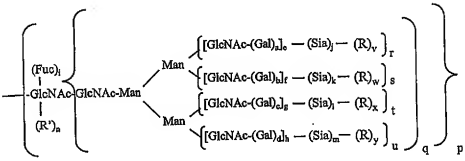
(h) prior to step (a), contacting the A-1-PI peptide with a member selected from a mannosidase, a xylosidase, a hexosaminidase and combinations thereof under conditions appropriate to remove a glycosyl residue from the A-1-PI peptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In other preferred embodiments and referring to the A-1PI peptide formula above, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; and e, f, g, and h are 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, q, r, s, t and u are members independently selected from 0 and 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and e, g, i, q, r, and t are members independently selected from 0 and 1. Alternatively, n, a, b, c, d, e, f, g, h, i, j, k, l, and m are 0; q, r, s, t, u, v, w, x, and y area members independently selected from 0 and 1; and p is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, n, p, and q are 0; r, s, t, u, v, w, x, and y are members independently selected from 0 and 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; p, v, w, x, and y are 0; and n and q are 1.

There is also provided an alpha 1 protease inhibitor peptide conjugate formed by the above-described method.

Also included in the invention is a method of forming a conjugate between a beta glucosidase peptide and a modifying group, wherein the modifying group is covalently attached to the beta glucosidase peptide through an intact glycosyl linking group, the beta glucosidase peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, n, p, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100; and

v, w, x, and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is H or a glycosyl residue, a glycoconjugate, or a modifying group.

The method comprises:

(a) contacting the beta glucosidase peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying

group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the beta glucosidase peptide with a sialidase under conditions appropriate to remove sialic acid from the beta glucosidase peptide.

In another embodiment, the method further comprises:

(c) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In yet another embodiment, the method comprises:

(d) prior to step (a) contacting the beta glucosidase peptide with a combination of a glycosidase and a sialidase.

In an additional embodiment, the method comprises:

(e) prior to step (a), contacting the beta glucosidase peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the beta glucosidase peptide.

Additionally, the method comprises:

(f) prior to step (a), contacting the beta glucosidase peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the beta glucosidase peptide.

Further, the method comprises:

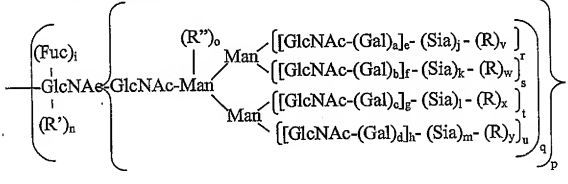
(g) prior to step (a), contacting the beta glucosidase peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer galactose to the product.

In another aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the beta glucosidase peptide formula described above, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; p, e, f, g, and h are 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; e, g, i, q, r, and t are members independently selected from 0 and 1; and p is 1. or, n, a, b, c, d, e, f, g, h, i, j, k, l, and m are 0; q, r, s, t, u, v, w, x, and y are members independently selected from 0 and 1; p is 1; and R is mannose or oligomannose.

The invention also includes a beta glucosidase peptide conjugate formed by the above described method.

The invention further provides a method of forming a conjugate between a tissue plasminogen activator (TPA) peptide and a modifying group, wherein the modifying group is covalently attached to the TPA peptide through an intact glycosyl linking group, the TPA peptide having a glycosyl subunit comprising the formula:



wherein

a, b, c, d, i, n, o, p, q, r, s, t, u, v, w, x and y are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers from 0 and 6;

j, k, l, and m are members independently selected from the integers from 0 and 100;

R is a modifying group, mannose or oligomannose;

R' is H or a glycosyl residue, a glycoconjugate, or a modifying group; and

R" is a glycosyl group, a glycoconjugate or a modifying group. The method comprises:

(a) contacting the TPA peptide with a member selected from a glycosyltransferase and a glycosidase operating synthetically and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method further comprises:

(b) prior to step (a), contacting the TPA peptide with a sialidase under conditions appropriate to remove sialic acid from the TPA peptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the TPA peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the TPA peptide.

In an additional embodiment, the method comprises:

(e) prior to step (a) contacting the TPA peptide with a combination of a glycosidase and a sialidase.

In yet another embodiment, the method comprises:

(f) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

In another embodiment, the method comprises:

(g) prior to step (a), contacting the TPA peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the TPA peptide.

In addition, the method comprises:

(h) prior to step (a), contacting the TPA peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the TPA peptide.

In yet another embodiment, the method comprises:

(i) prior to step (a), contacting the TPA peptide with a member selected from a mannosidase, a xylosidase, a hexosaminidase and combinations thereof under conditions appropriate to remove a glycosyl residue from the TPA peptide.

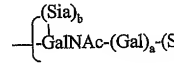
In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the TPA peptide formula described above, a, b, c, d are 1; e, f, g and h are members selected from the integers between 1 and 3; i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; and n, o, v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, n, o, s, u, v, w, x, and y are 0; e, g, i, r, and t are members independently selected from 0 and 1; and q and p are 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, p, q, r, s, t, and u are members independently selected from 0 and 1; and n, o, v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, and p are 1; h is a member selected from the integers between 1 and 3; j, k, l, m, i, q, r, s, t, and u are members independently selected from 0 and 1; and n, o, v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; e, g, i, q, r, and t are members independently selected from 0 and 1; o is 1; and R" is xylose. Alternatively, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; e, f, g, and h are 1; and n, o, v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, r, s, t, u, v, w, x, and y are 0; i and q are members independently selected from 0 and 1; and p is 1. Alternatively, a, b, c, d, e, f, g, h, j,

k, l, m, o, r, s, t, u, v, w, x, and y are 0; i and q are members independently selected from 0 and 1; p is 0; and n is 1.

Also included is a TPA peptide conjugate formed by the above described method.

The invention also provides a method of forming a conjugate between an interleukin 2 (IL-2) peptide and a modifying group, wherein the modifying group is covalently attached to the IL-2 peptide through an intact glycosyl linking group, the IL-2 peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, and e are members independently selected from 0 and 1;

d is 0; and

R is a modifying group. The method comprises:

(a) contacting the IL-2 peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method further comprises:

(b) prior to step (a), contacting the IL-2 peptide with a sialidase under conditions appropriate to remove sialic acid from the IL-2 peptide.

In another embodiment, the method comprises:

(c) prior to step (a), contacting the IL-2 peptide with an endo-N-acetylgalactosaminidase operating synthetically under conditions appropriate to add a GalNAc to the IL-2 peptide.

In yet an additional embodiment, the method comprises:

(d) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

Further, the method comprises:

(e) prior to step (a), contacting the IL-2 peptide with N-acetylgalactosamine transferase and a GalNAc donor under conditions appropriate to transfer GalNAc to the IL-2 peptide.

In addition, the method comprises:

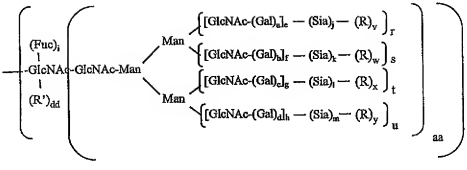
(f) prior to step (a) contacting the IL-2 peptide with galactosyltransferase and a galactose donor under conditions appropriate to transfer galactose to the IL-2 peptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

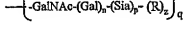
In preferred embodiments and referring to the IL-2 peptide formula described above, a and e are members independently selected from 0 and 1; and b, c, and d are 0. Alternatively, a, b, c, d, and e are 0.

The invention additionally includes an IL-2 peptide conjugate formed by the above described method.

Also included in the invention is a method of forming a conjugate between a Factor VIII peptide and a modifying group, wherein the modifying group is covalently attached to the glycopeptide through an intact glycosyl linking group, the glycopeptide comprising a glycosyl residue having a formula which is a member selected from:



and



wherein

a, b, c, d, i, n, o, p, q, r, s, t, u, aa, cc, and dd are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 20;

v, w, x, y and z are 0; and

R is a modifying group, a mannose or an oligomannose;

R' is a member selected from H, a glycosyl residue, a modifying group and a glycoconjugate. The method comprises:

(a) contacting the glycopeptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the glycopeptide with a sialidase under conditions appropriate to remove sialic acid from the glycopeptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In an additional embodiment, the method comprises:

(d) prior to step (a), contacting the glycopeptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the glycopeptide.

Also, the method comprises:

(e) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

Further, the method comprises:

(f) prior to step (a), contacting the glycopeptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the glycopeptide.

In addition, the method comprises:

(g) prior to step (a), contacting the glycopeptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

The method also comprises:

(h) prior to step (a), contacting the glycopeptide with ST3Gal3 and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

Moreover, the method comprises:

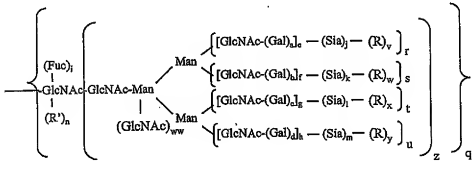
(i) prior to step (a), contacting the glycopeptide with a mannosidase under conditions appropriate to remove mannose from the glycopeptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the Factor VIII peptide formula described above, e, f, g, and h are members independently selected from the integers between 1 and 4; a, b, c, d, i, j, k, l, m, n, o, p, q, r, s, t, u, aa, and cc are members independently selected from 0 and 1; and v, w, x, y, z, and dd are 0.

There is also provided a Factor VIII peptide conjugate formed by the above described method.

Further provided in the invention is a method of forming a conjugate between a tumor necrosis factor (TNF) alpha receptor/IgG fusion peptide and a modifying group, wherein the modifying group is covalently attached to the glycopeptide through an intact glycosyl linking group, the glycopeptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, j, k, l, m, q, r, s, t, u, w, ww, and z are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 4;

n, v, x, and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is a member selected from H, a glycosyl residue, a modifying group and a glycoconjugate. The method comprises:

(a) contacting the glycopeptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the glycopeptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the glycopeptide.

In another embodiment, the method comprises:

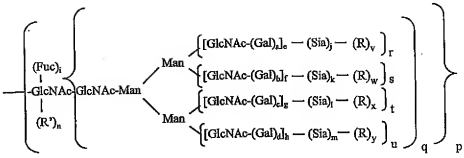
(c) prior to step (a), contacting the glycopeptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the TNF alpha receptor/IgG fusion peptide formula presented above, a, c, i, j, and l are members independently selected from 0 and 1; e, g, q, r, t, and z are 1; and b, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0. Alternatively, e, g, i, r, and t are members independently selected from 0 and 1; a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and q and z are 1.

There is also provided a TNF alpha receptor/IgG fusion peptide conjugate formed by the above described method.

The invention also includes a method of forming a conjugate between a urokinase peptide and a modifying group, wherein the modifying group is covalently attached to the urokinase peptide through an intact glycosyl linking group, the urokinase peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, n, p, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is H or a glycosyl residue, a glycoconjugate, or a modifying group.

The method comprises:

(a) contacting the urokinase peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the urokinase peptide with a sialidase under conditions appropriate to remove sialic acid from the urokinase peptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the urokinase peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the urokinase peptide.

In a further embodiment, the method comprises:

(e) prior to step (a) contacting the urokinase peptide with a combination of a glycosidase and a sialidase.

In yet another embodiment, the method comprises:

(f) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

Additionally, the method comprises:

(g) prior to step (a), contacting the urokinase peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the urokinase peptide.

Further, the method comprises:

(h) prior to step (a), contacting the urokinase peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the urokinase peptide.

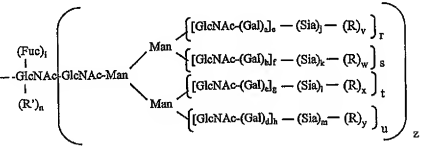
In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the urokinase peptide formula described above, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; e, f, g, and h are 1; v, w, x, and y are 0; and p is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; n, v, w, x, and y are 0; and p is 1. Alternatively, a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and

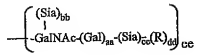
e, g, i, q, r, and t are members independently selected from 0 and 1; and p is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, r, s, t, u, v, w, x and y are 0; i is 0 or 1; and q and p are 1. Alternatively, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; e, f, g, and h are independently selected from 0, 1 ,2, 3 and 4; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, o, r, s, t, u, v, w, x and y are 0; q is 1; and n is 0 or 1.

Also provided is a urokinase peptide conjugate formed by the above described method.

The invention also includes a method of forming a conjugate between an anti-glycoprotein IIb/IIIa monoclonal antibody peptide and a modifying group, wherein the modifying group is covalently attached to the glycopeptide through an intact glycosyl linking group, the glycopeptide comprising a glycosyl residue having a formula which is a member selected from:



; and



wherein

a, b, c, d, i, j, k, l, m, r, s, t, u, z, aa, bb, cc, and ee are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers from 0 and 4;

n, v, w, x, y, and dd are 0;

R is a modifying group a mannose or an oligomannose; and

R^1 is a member selected from H, a glycosyl residue, a modifying group and a glycoconjugate. The method comprises:

(a) contacting the glycopeptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the glycopeptide with a sialidase under conditions appropriate to remove sialic acid from the glycopeptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the glycopeptide with a galactosidase operating synthetically under conditions appropriate to add a galactose to the glycopeptide.

In a further embodiment, the method comprises:

(e) prior to step (a), contacting the glycopeptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the glycopeptide.

In addition, the method comprises:

(f) contacting the product from step (e) with ST3Gal3 and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

Further, the method comprises:

(g) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

Also, the method comprises:

(h) prior to step (a), contacting the glycopeptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the glycopeptide.

Moreover, the method comprises:

(i) prior to step (a), contacting the glycopeptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

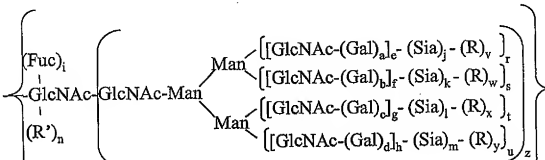
In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the anti-glycoprotein IIb/IIIa monoclonal antibody peptide formula described above, a, b, c, d, e, f, g, h, i, j, k, l, m r, s, t, and u are members independently selected from 0 and 1; n, v, w, x, and y are 0; and z is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, s, t, u, v, w, x, and y are 0; i and r are members independently selected from 0 and 1; and z is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, and n are 0; r, s, t, u, v, w, x, and y are members independently selected from 0 and 1; and z is 1. Alternatively, aa, bb, cc, and ee are members independently selected from 0 and 1; and dd is 0. Alternatively, aa and ee are members independently selected from 0 and 1; and bb, cc, and dd are 0. Alternatively, aa, bb, cc, dd, and ee are 0.

Also provided is an anti-glycoprotein IIb/IIIa monoclonal antibody peptide conjugate formed by the above described method.

There is further provided in the invention a method of forming a conjugate between a chimeric anti-HER2 antibody peptide and a modifying group, wherein the

modifying group is covalently attached to the chimeric anti-HER2 antibody peptide through an intact glycosyl linking group, the chimeric anti-HER2 antibody peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, j, k, l, q, r, s, t, u, and z are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 4;

n, v, w, x, and y are 0;

m is 0-20;

R is a modifying group, a mannose or an oligomannose; and

R' is a member selected from hydrogen and a glycosyl residue, and a modifying group. the method comprises:

(a) contacting the chimeric anti-HER2 antibody peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the chimeric anti-HER2 antibody peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the chimeric anti-HER2 antibody peptide.

In another embodiment, the method comprises:

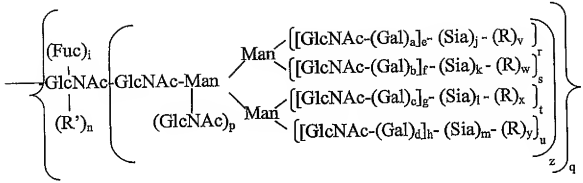
(c) prior to step (a), contacting the chimeric anti-HER2 antibody peptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the chimeric anti-HER2 antibody peptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

In preferred embodiments and referring to the anti-HER2 antibody peptide formula described above, a, c, and i are members independently selected from 0 and 1; e, g, r, and t are 1; b, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and q and z are 1. Alternatively, i is 0 or 1; q and z are 1; and a, b, c, d, e, f, g, h, j, k, l, m, n, r, s, t, u, v, w, x, and y are 0. Alternatively, e, g, i, r, and t are members independently selected from 0 and 1; a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and q and z are 1.

Also provided is an anti-HER2 antibody peptide conjugate formed by the above described method.

The invention further provides method of forming a conjugate between an anti-RSV F peptide and a modifying group, wherein the modifying group is covalently attached to the anti-RSV F peptide through an intact glycosyl linking group, the anti-RSV F peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, j, k, l, m, p, q, r, s, t, u, and z are members independently selected from 0 and 1;

e, f, g and h are members independently selected from the integers from 0 to 4;

n, v, w, x and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is a member selected from H and a glycosyl residue, a glycoconjugate, and a modifying group. The method comprises:

(a) contacting the anti-RSV F peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the anti-RSV F peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the anti-RSV F peptide.

In another embodiment, the method comprises:

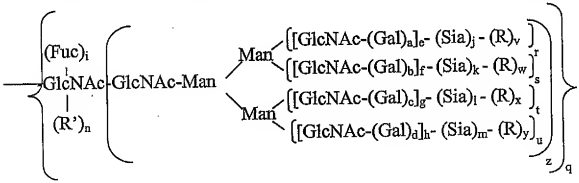
(c) prior to step (b), contacting the anti-RSV F peptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the anti-RSV F peptide.

In preferred embodiments and referring to the anti-RSV F peptide formula presented above, a, c, e, g and i are members independently selected from 0 and 1; r and t are 1; b, d, f, h, j, k, l, m, n, s, u, v, w, x and y are 0; and z is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, r, s, t, u, v, w, x, y are 0; i and p are independently selected from 0 or 1; q and z are 1; and n is 0. Alternatively, e, g, i, r and t are members independently selected from 0 and 1; a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x and y are 0; and q and z are 1.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

Also provided is an anti RSV F peptide conjugate formed by the above described method.

Also included in the invention is a method of forming a conjugate between an anti-CD20 antibody peptide and a modifying group, wherein the modifying group is covalently attached to the anti-CD20 antibody peptide through an intact glycosyl linking group, the anti-CD20 antibody peptide having a glycosyl subunit comprising the formula:



wherein

a, b, c, d, i, j, k, l, m q, r, s, t, u and z are integers independently selected from 0 and 1;

e, f, g, and h are independently selected from the integers from 0 to 4;

n, v, w, x, and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is a member selected from H, a glycosyl residue, a glycoconjugate or a modifying group. The method comprises:

(a) contacting the anti-CD20 antibody peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the anti-CD20 antibody peptide with a galactosyltransferase and a galactosyl donor under conditions appropriate for the transfer of the galactosyl donor to the anti-CD20 antibody peptide.

In another embodiment, the method comprises:

(c) prior to step (b), contacting the anti-CD20 antibody peptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the anti-CD20 antibody peptide.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the anti-CD20 antibody peptide with a mannosidase under conditions appropriate to remove mannose from the anti-CD20 antibody peptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

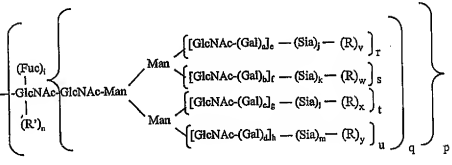
In another aspect, the glycosyltransferase is galactosyltransferase and the modified glycosyl donor is a modified galactosyl donor.

In preferred embodiments and referring to the anti-CD20 peptide formula presented above, a, c, e, g and i are members independently selected from 0 and 1; r, t, q and z are 1; and b, d, f, h, j, k, l, m, n, s, u, v, w, x and y are 0. Alternatively, a, c, e, g, i, q, r, and

t are members independently selected from 0 and 1; b, d, f, h, j, k, l, m, s, u, v, w, x, y are 0; and z is 1. Alternatively, e, g, i, q, r, and t are members independently selected from 0 and 1; a, b, c, d, f, h, j, k, l, m, n, s, u, v, w, x, and y are 0; and z is 1. Alternatively, i is 0 or 1; q and z are 1; and a, b, c, d, e, f, g, h, j, k, l, m, n, r, s, t, u, v, w, x and y are 0. Alternatively, e, g, i, r, t, v, x and z are members independently selected from 0 and 1; a, b, c, d, f, h, j, k, l, m, n, s, u, w and y are 0; and z is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, r, s, t, u, v, w, x and y are 0; n and q are 1; and i is 0 or 1.

Also included is an anti-CD20 antibody peptide conjugate formed by the above-described method.

The invention additionally provides a method of forming a conjugate between a recombinant DNase peptide and a modifying group, wherein the modifying group is covalently attached to the recombinant DNase peptide through an intact glycosyl linking group, the recombinant DNase peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, n, p q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 100;

v, w, x, and y are 0; and

R is a member selected from polymer, a glycoconjugate, a mannose, an oligomannose and a modifying group. The method comprises:

(a) contacting the recombinant DNase peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the recombinant DNase peptide with a sialidase under conditions appropriate to remove sialic acid from the recombinant DNase peptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In an additional embodiment, the method comprises:

(d) prior to step (a), contacting the recombinant DNase peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the recombinant DNase peptide.

In yet a further embodiment, the method comprises:

(e) prior to step (a) contacting the recombinant DNase peptide with a combination of a glycosidase and a sialidase.

In another embodiment, the method comprises:

(f) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

The method also comprises:

(g) prior to step (a), contacting the recombinant DNase peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the recombinant DNase peptide.

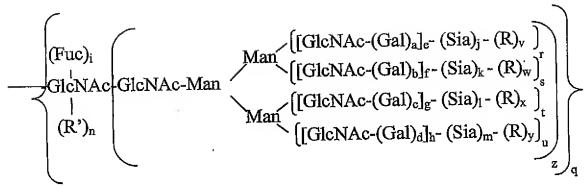
In addition, the method comprises:

(h) prior to step (a), contacting the recombinant DNase peptide with an endoglycanase under conditions appropriate to cleave a glycosyl moiety from the recombinant DNase peptide.

In preferred embodiments and referring to the DNase peptide formula presented above, a, b, c, d, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; e, f, g, h and p are 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, q, r, s, t, and u are members independently selected from 0 and 1; p is 1; and n, v, w, x, and y are 0. Alternatively, a, b, c, d, f, h, j, k, l, m, s, u, v, w, x, and y are 0; and e, g, i, q, r, and t are members independently selected from 0 and 1; and p is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, r, s, t, u, v, w, x, and y are 0; i is 0 or 1; and p is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l and m are 0; i, q, r, s, t, u, v, x and y are independently selected from 0 or 1; p is 1; and R is mannose or oligomannose.

Also provided is a recombinant DNase peptide conjugate formed by the above described method.

The invention additionally includes a method of forming a conjugate between an anti-tumor necrosis factor (TNF) alpha peptide and a modifying group, wherein the modifying group is covalently attached to the anti-TNF alpha peptide through an intact glycosyl linking group, the anti-TNF alpha peptide comprising a glycosyl residue having the formula:



wherein

a, b, c, d, i, n, o, p, q, r, s, t, u and z are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

j, k, l, and m are members independently selected from the integers between 0 and 20;

n, v, w, x and y are 0; and

R is a modifying group, a mannose or an oligomannose;

R' is a glycoconjugate or a modifying group. The method comprises:

(a) contacting the anti-TNF alpha peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the anti-TNF alpha peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the anti-TNF alpha peptide.

In another embodiment, the method comprises:

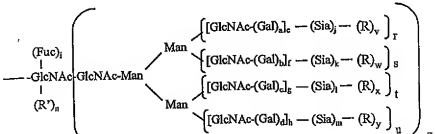
(c) prior to step (a), contacting the anti-TNF alpha peptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the anti-TNF alpha peptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

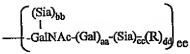
In preferred embodiments and referring to the anti-TNF alpha peptide formula presented above, a, b, c, d, e, f, g, h, i, j, k, l, m, o, p, q, r, s, t and u are members independently selected from 0 and 1; n is 1; and v, w, x, y, and z are 0. Alternatively, a, c, e, g and i are members independently selected from 0 and 1; r and t are 1; b, d, f, h, j, k, l, m, n, s, u, v, w, x and y; and q and z are 1.

Also included is an anti-TNF alpha peptide conjugate formed by the above described method.

The invention also provides a method of forming a conjugate between an insulin peptide and a modifying group, wherein the modifying group is covalently attached to the glycopeptide through an intact glycosyl linking group, the glycopeptide comprising a glycosyl residue having a formula which is a member selected from:



; and



wherein

a, b, c, d, i, j, k, l, m, r, s, t, u, z, aa, bb, cc, and ee are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integer between 0 and 4;

dd, n, v, w, x and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is a member selected from H, a glycosyl residue, a modifying group and a glycoconjugate. The method comprises:

(a) contacting the glycopeptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the glycopeptide with a sialidase under conditions appropriate to remove sialic acid from the glycopeptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the glycopeptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the glycopeptide.

In a further embodiment, the method comprises:

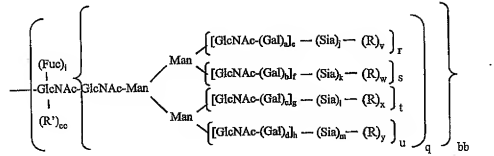
(e) prior to step (a), contacting the glycopeptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety and a glycoconjugate.

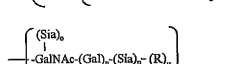
In preferred embodiments and referring to the insulin peptide formula presented above, a, b, c, d, e, f, g, h, i, j, k, l, m, r, s, t, and u are members independently selected from 0 and 1; n, v, w, x, and y are 0; and z is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, s, t, u, v, w, x, and y are 0; i and r are members independently selected from 0 and 1; and z is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, and n are 0; r, s, t, u, v, w, x, and y are members independently selected from 0 and 1; and z is 1. Alternatively, aa, bb, cc, and ee are members independently selected from 0 and 1; and dd is 0. Alternatively, aa and ee are members independently selected from 0 and 1; and bb, cc, and dd are 0. Alternatively, aa, bb, cc, dd, and ee are 0.

The invention further includes an insulin peptide conjugate formed by the above described method.

In addition, there is provided in the invention a method of forming a conjugate between a hepatitis B surface antigen (HBsAg) peptide and a modifying group, wherein the modifying group is covalently attached to the HBsAg peptide through an intact glycosyl linking group, the HBsAg peptide comprising a glycosyl residue having a formula which is a member selected from:



; and



wherein

aa, bb, a, b, c, d, i, n, q, r, s, t, and u are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 6;

o, p, j, k, l, and m are members independently selected from the integers between 0 and 100;

cc, v, w, x, and y are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is H or a glycosyl residue, a glycoconjugate, or a modifying group.

The method comprises :

(a) contacting the HBsAg peptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In one embodiment, the method comprises:

(b) prior to step (a), contacting the HBsAg peptide with a sialidase under conditions appropriate to remove sialic acid from the HBsAg peptide.

In another embodiment, the method comprises:

(c) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In yet another embodiment, the method comprises:

(d) prior to step (a), contacting the HBsAg peptide with a galactosidase under conditions appropriate to cleave a glycosyl residue from the HBsAg peptide.

The method also comprises:

(e) prior to step (a), contacting the HBsAg peptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the HBsAg peptide.

In addition, the method comprises:

(f) contacting the product of step (d) with ST3Gal3 and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

Also, the method comprises:

(g) contacting the product from step (a) with a moiety that reacts with the modifying group, thereby forming a conjugate between the intact glycosyl linking group and the moiety.

Also, the method comprises:

(h) prior to step (a), contacting the HBsAg peptide with N-acetylglucosamine transferase and a GlcNAc donor under conditions appropriate to transfer GlcNAc to the HBsAg peptide.

In addition, the method comprises:

(i) prior to step (a), contacting the HBsAg peptide with a mannosidase under conditions appropriate to cleave mannose from the HBsAg peptide.

Also, the method comprises:

(j) prior to step (a), contacting the HBsAg peptide with endoglycanase under conditions sufficient to cleave a glycosyl group from the HBsAg peptide.

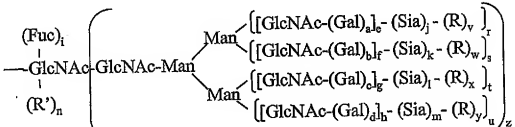
In one aspect, the modifying group is a member selected from a polymer, a toxin, a radioisotope, a therapeutic moiety, an adjuvant and a glycoconjugate.

In preferred embodiments and referring to the HBsAg peptide formula presented above, a, b, c, d, i, j, k, l, m, o, p, q, r, s, t, u, and aa are members independently selected from 0 and 1; bb, e, f, g, h, and n are 1; and cc, v, w, x, y, and z are 0. Alternatively, a, b, c, d, i, j, k, l, m, n, o, p, q, r, s, t, u, and aa are members independently selected from 0 and 1; e, f, g, and h are independently selected from 0, 1, 2, 3, or 4; cc, v, w, x, y, and z are 0; and bb is 1. Alternatively, cc, a, b, c, d, e, f, g, h, i, j, k, l, m, n, o, p, v, w, x, y and z are 0; and q, r, s, t, u, v, w, x, y, and aa are members independently selected from 0 and 1; and bb is 1. Alternatively, a, b, c, d, i, j, k, l, m, o, q, r, s, t, u, and aa are members independently selected from 0 and 1; bb, e, f, g, h, and n are 1; and n, p cc, v, w, x, y, and z are 0.

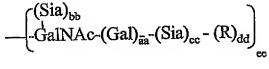
Alternatively, bb, a, b, c, d, e, f, g, h, i, j, k, l, m, o, p, q, r, s, t, u, v, w, x, y, and z are members independently selected from 0 and 1; cc is 1; and n is 0 or 1. Alternatively, a, b, c, d, f, h, j, k, l, m, o, p, s, u, v, w, x, y, z, and cc are 0; bb is 1; e, g, i, n, q, r, t, and aa are members independently selected from 0 and 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, n, o, p, z, and cc are 0; q, r, s, t, u, v, w, x, y, and aa are members independently selected from 0 and 1; and bb is 1.

Also included is a HBsAg peptide conjugate formed by the above described method.

The invention further provides a method of forming a conjugate between a human growth hormone (HGH) peptide and a modifying group, wherein the modifying group is covalently attached to the glycopeptide through an intact glycosyl linking group, the glycopeptide comprising a glycosyl residue having a formula which is a member selected from:



; and



wherein

a, b, c, d, i, j, k, l, m, r, s, t, u, z, aa, bb, cc, and ee are members independently selected from 0 and 1;

e, f, g, and h are members independently selected from the integers between 0 and 4;

n, v, w, x, y, and dd are 0;

R is a modifying group, a mannose or an oligomannose; and

R' is a member selected from H, a glycosyl residue, a modifying group and a glycoconjugate. The method comprises:

(a) contacting the glycopeptide with a glycosyltransferase and a modified glycosyl donor, comprising a glycosyl moiety which is a substrate for the glycosyltransferase covalently bound to the modifying group, under conditions appropriate for the formation of the intact glycosyl linking group.

In another embodiment, the method comprises:

(b) prior to step (a), contacting the glycopeptide with a sialidase under conditions appropriate to remove sialic acid from the glycopeptide.

In one embodiment, the method comprises:

(c) prior to step (a), contacting the glycopeptide with endoglycanase under conditions appropriate to cleave a glycosyl moiety from the glycopeptide.

In another embodiment, the method comprises:

(c) prior to step (a), contacting the glycopeptide with a galactosyl transferase and a galactose donor under conditions appropriate to transfer the galactose to the glycopeptide.

In yet another embodiment, the method comprises:

(d) contacting the product of step (a) with a sialyltransferase and a sialic acid donor under conditions appropriate to transfer sialic acid to the product.

In a further embodiment, the method comprises:

(d) prior to step (a), contacting the glycopeptide with a galactosidase under conditions appropriate to cleave a glycosyl residue from the glycopeptide.

In preferred embodiments and referring to the HGH peptide formula presented above, a, b, c, d, e, f, g, h, i, j, k, l, m, r, s, t, and u are members

independently selected from 0 and 1; n, v, w, x, and y are 0; and z is 1. Alternatively, a, b, c, d, e, f, g, h, j, k, l, m, n, s, t, u, v, w, x, and y are 0; i and r are members independently selected from 0 and 1; and z is 1. Alternatively, a, b, c, d, e, f, g, h, i, j, k, l, m, and n are 0; r, s, t, u, v, w, x and y are members independently selected from 0 and 1; and z is 1. Alternatively, aa and ee are members independently selected from 0 and 1; and bb, cc, and dd are 0. Alternatively, aa, bb, cc, dd, and ee are 0. Alternatively, aa, bb, cc, dd, ee, and n are 0.

Also included is a HGH peptide conjugate formed by the above described method.

BRIEF DESCRIPTION OF THE DRAWINGS

For the purpose of illustrating the invention, there are depicted in the drawings certain embodiments of the invention. However, the invention is not limited to the precise arrangements and instrumentalities of the embodiments depicted in the drawings.

Figure 1, comprising Figure 1A to Figure 1Z and Figure 1AA to Figure 1CC, is a list of peptides useful in the methods of the invention.

Figure 2 is a scheme depicting a trimannosyl core glycan (left side) and the enzymatic process for the generation of a glycan having a bisecting GlcNAc (right side).

Figure 3 is a scheme depicting an elemental trimannosyl core structure and complex chains in various degrees of completion. The *in vitro* enzymatic generation of an elemental trimannosyl core structure from a complex carbohydrate glycan structure which does not contain a bisecting GlcNAc residue is shown as is the generation of a glycan structure therefrom which contains a bisecting GlcNAc. Symbols: squares: GlcNAc; light circles: Man; dark circles: Gal; triangles: NeuAc.

Figure 4 is a scheme for the enzymatic generation of a sialylated glycan structure (right side) beginning with a glycan having a trimannosyl core and a bisecting GlcNAc (left side).

Figure 5 is a scheme of a typical high mannose containing glycan structure (left side) and the enzymatic process for reduction of this structure to an elemental trimannosyl core structure.

Figure 6 is a diagram of a fucose and xylose containing N-linked glycan structure typically produced in plant cells.

Figure 7 is a diagram of a fucose containing N-linked glycan structure typically produced in insect cells.

Figure 8 is a scheme depicting a variety of pathways for the trimming of a high mannose structure and the synthesis of complex sugar chains therefrom. Symbols: squares: GlcNAc; circles: Man; diamonds: fucose; pentagon: xylose.

Figure 9 is a scheme depicting *in vitro* strategies for the synthesis of complex structures from an elemental trimannosyl core structure. Symbols: Dark squares: GlcNAc; light circles: Man; dark circles: Gal; dark triangles: NeuAc; GnT: N-acetyl glucosaminyltransferase; GalT: galactosyltransferase; ST: sialyltransferase.

Figure 10 is a scheme depicting various complex structures which may be synthesized from an elemental trimannosyl core structure. Symbols: Dark squares: GlcNAc; light circles: Man; dark circles: Gal; dark triangles: NeuAc; dark diamonds: fucose; FT and FucT: fucosyltransferase; GalT: galactosyltransferase; ST: sialyltransferase; Le: Lewis antigen; SLe: sialylated Lewis antigen.

Figure 11 is an exemplary scheme for preparing O-linked glycopeptides originating with serine or threonine.

Figure 12 is a series of diagrams depicting the four types of O-glycan structure, termed cores 1 through 4. The core structure is outlined in dotted lines.

Figure 13, comprising Figure 13A and Figure 13B, is a series of schemes showing an exemplary embodiment of the invention in which carbohydrate residues comprising complex carbohydrate structures and/or high mannose high mannose structures are trimmed back to the first generation biantennary structure. A modified sugar bearing a water soluble polymer (WSP) is then conjugated to one or more of the sugar residues exposed by the trimming back process.

Figure 14 is a scheme similar to that shown in Figure 2, in which a high mannose structure is "trimmed back" to the mannose from which the biantennary structure branches

and a modified sugar bearing a water soluble polymer is then conjugated to one or more of the sugar residues exposed by the trimming back process.

Figure 15 is a scheme similar to that shown in Figure 2, in which high mannose is trimmed back to the GlcNAc to which the first mannose is attached, and a modified sugar bearing a water soluble polymer is then conjugated to one or more of the sugar residues exposed by the trimming back process.

Figure 16 is a scheme similar to that shown in Figure 2, in which high mannose is trimmed back to the first GlcNAc attached to the Asn of the peptide, following which a water soluble polymer is conjugated to one or more sugar residues which have subsequently added on.

Figure 17, comprising Figure 17A and 17B, is a scheme in which a N-linked carbohydrate is trimmed back and subsequently derivatized with a modified sugar moiety (GlcNAc) bearing a water-soluble polymer.

Figure 18, comprising Figure 18A and 18B, is a scheme in which a N-linked carbohydrate is trimmed back and subsequently derivatized with a sialic acid moiety bearing a water-soluble polymer.

Figure 19 is a scheme in which a N-linked carbohydrate is trimmed back and subsequently derivatized with one or more sialic acid moieties, and terminated with a sialic acid derivatized with a water-soluble polymer.

Figure 20 is a scheme in which an O-linked saccharide is "trimmed back" and subsequently conjugated to a modified sugar bearing a water soluble polymer. In the exemplary scheme, the carbohydrate moiety is "trimmed back" to the first generation of the biantennary structure.

Figure 21 is an exemplary scheme for trimming back the carbohydrate moiety of an O-linked glycopeptide to produce a mannose available for conjugation with a modified sugar having a water-soluble polymer attached thereto.

Figure 22, comprising Figure 22A to Figure 22C, is a series of exemplary schemes. Figure 22A is a scheme that illustrates addition of a PEGylated sugar, followed by the addition of a non-modified sugar. Figure 22B is a scheme that illustrates the addition of more that one kind of modified sugar onto on one glycan. Figure 22C is a scheme that illustrates the addition of different modified sugars onto O-linked glycans and N-linked glycans.

Figure 23 is a diagram of various methods of improving the therapeutic function of a peptide by glycan remodeling, including conjugation.

Figure 24 is a set of schemes for glycan remodeling of a therapeutic peptide to treat Gaucher's Disease.

Figure 25 is a scheme for glycan remodeling to generate glycans having a terminal mannose-6-phosphate moiety.

Figure 26 is a diagram illustrating the array of glycan structures found on CHO-produced glucocerebrosidase (Cerezyme™) after sialylation.

Figure 27, comprising Figures 27A to 27G, provides exemplary schemes for remodeling glycan structures on granulocyte colony stimulating factor (G-CSF). Figure 27A is a diagram depicting the G-CSF peptide indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 27B to 27G are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 27A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 28, comprising Figures 28A to 28AA sets forth exemplary schemes for remodeling glycan structures on interferon-alpha. Figure 28A is a diagram depicting the interferon-alpha isoform 14c peptide indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 28B to 28D are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 28A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 28E is a diagram depicting the interferon-alpha isoform 14c peptide indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 28F to 28N are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 28E based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 28O is a diagram depicting the interferon-alpha isoform 2a or 2b peptides indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 28P to 28W are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 28O based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 28X is a diagram depicting the interferon-alpha-mucin fusion peptides indicating the residue(s) which binds to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 28Y to 28AA are

diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 28X based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 28BB is a diagram depicting the interferon-alpha-mucin fusion peptides and interferon-alpha peptides indicating the residue(s) which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 28CC to 28EE are diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 28BB based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 29, comprising Figures 29A to 29S, sets forth exemplary schemes for remodeling glycan structures on interferon-beta. Figure 29A is a diagram depicting the interferon-beta peptide indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 29B to 29O are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 29A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 29P is a diagram depicting the interferon-beta peptide indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 29Q to 29S are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 29P based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 30, comprising Figures 30A to 30D, sets forth exemplary schemes for remodeling glycan structures on Factor VII and Factor VIIa. Figure 30A is a diagram depicting the Factor-VII and Factor-VIIa peptides A (solid line) and B (dotted line) indicating the residues which bind to glycans contemplated for remodeling, and the formulas for the glycans. Figure 30B to 30D are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 30A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 31, comprising Figures 31A to 31G, sets forth exemplary schemes for remodeling glycan structures on Factor IX. Figure 31A is a diagram depicting the Factor-IX peptide indicating residues which bind to glycans contemplated for remodeling, and formulas of the glycans. Figure 31B to 31G are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 31A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 32, comprising Figures 32A to 32J, sets forth exemplary schemes for remodeling glycan structures on follicle stimulating hormone (FSH), comprising α and β subunits. Figure 32A is a diagram depicting the Follicle Stimulating Hormone peptides FSHα and FSHβ indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 32B to 32J are diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 32A based on the type of cell the peptides are expressed in and the desired remodeled glycan structures.

Figure 33, comprising Figures 33A to 33J, sets forth exemplary schemes for remodeling glycan structures on Erythropoietin (EPO). Figure 33A is a diagram depicting the EPO peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 33B to 33J are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 33A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 34, comprising Figures 34A to 34K sets forth exemplary schemes for remodeling glycan structures on Granulocyte-Macrophage Colony Stimulating Factor (GM-CSF). Figure 34A is a diagram depicting the GM-CSF peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 34B to 34G are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 34A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 34H is a diagram depicting the GM-CSF peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 34I to 34K are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 34H based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 35, comprising Figures 35A to 35N, sets forth exemplary schemes for remodeling glycan structures on interferon-gamma. Figure 35A is a diagram depicting an interferon-gamma peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 35B to 35G are diagrams of contemplated remodeling steps of the peptide in Figure 35A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 35H is a diagram depicting an interferon-gamma peptide indicating the residues which bind to glycans

contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 35I to 35N are diagrams of contemplated remodeling steps of the peptide in Figure 35H based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 36, comprising Figures 36A to 36O, sets forth exemplary schemes for remodeling glycan structures on α_1-antitrypsin (ATT, or α-1 protease inhibitor). Figure 36A is a diagram depicting an AAT peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 36B to 36G are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 36A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 36H is a diagram depicting an AAT peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 36I to 36K are diagrams of contemplated remodeling steps of the peptide in Figure 36H based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 36L is a diagram depicting an AAT peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 36M to 36O are diagrams of contemplated remodeling steps of the peptide in Figure 36L based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 37, comprising Figures 37A to 37K sets forth exemplary schemes for remodeling glycan structures on glucocerebrosidase. Figure 37A is a diagram depicting the glucocerebrosidase peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 37B to 37G are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 37A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 37H is a diagram depicting the glucocerebrosidase peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 37I to 37K are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 37H based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 38, comprising Figures 38A to 38W, sets forth exemplary schemes for remodeling glycan structures on Tissue-Type Plasminogen Activator (TPA). Figure 38A is a

diagram depicting the TPA peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 38B to 38G are diagrams of contemplated remodeling steps of the peptide in Figure 38A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 38H is a diagram depicting the TPA peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 38I to 38K are diagrams of contemplated remodeling steps of the peptide in Figure 38H based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 38L is a diagram depicting a mutant TPA peptide indicating the residues which bind to glycans contemplated for remodeling, and the formula for the glycans. Figure 38M to 38O are diagrams of contemplated remodeling steps of the peptide in Figure 38L based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 38P is a diagram depicting a mutant TPA peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 38Q to 38S are diagrams of contemplated remodeling steps of the peptide in Figure 38P based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 38T is a diagram depicting a mutant TPA peptide indicating the residues which binds to glycans contemplated for remodeling, and formulas for the glycans. Figure 38U to 38W are diagrams of contemplated remodeling steps of the peptide in Figure 38T based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 39, comprising Figures 39A to 39G, sets forth exemplary schemes for remodeling glycan structures on Interleukin-2 (IL-2). Figure 39A is a diagram depicting the interleukin-2 peptide indicating the amino acid residue to which a glycan binds, and an exemplary glycan formula bound thereto. Figure 39B to 39G are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 39A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 40, comprising Figures 40A to 40N, sets forth exemplary schemes for remodeling glycan structures on Factor VIII. Figure 40A are the formulas for the glycans that bind to the N-linked glycosylation sites (A and A') and to the O-linked sites (B) of the Factor VIII peptides. Figure 40B to 40F are diagrams of contemplated remodeling steps of the peptides in Figure 40A based on the type of cell the peptide is expressed in and the